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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:05 ; Search time 11 Seconds
(without alignments)
94.264 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GWAALPRLIAFTSEHSFSLKKGAA 25

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database : SwissProt_40*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.0	21	1 MISG MISAN	P81474 Misgurnus a
2	5	20.0	24	1 FRA4 LITIN	P82023 litoria inf
3	4	16.0	8	1 GLUR HUMAN	P02729 homo sapien
4	4	16.0	19	1 ATPB CANFA	P99504 canis fami
5	4	16.0	22	1 CUSP TRIVA	P3404 trichomonas
6	4	16.0	23	1 ALLS HORSE	P82616 equus cabal
7	4	16.0	23	1 FLAI SULSH	Q8UW96 sulfolobus
8	4	16.0	23	1 RR19 PETHY	P18550 petunia hyb
9	4	16.0	24	1 PCW5 PACGO	P82427 pachycondyl
10	3	12.0	8	1 CAD1 ENTEA	P13268 enterococcu
11	3	12.0	8	1 LMT2 LOEMI	P22396 locusta mig
12	3	12.0	8	1 LFK LEUMA	P13049 leucophaea
13	3	12.0	8	1 ORMY ORCLI	P82455 orconectes
14	3	12.0	8	1 PKP2 PERAM	P82692 periplaneta
15	3	12.0	8	1 PKP3 PERAM	P82618 periplaneta
16	3	12.0	9	1 CCAP CARNA	P38556 carcinus ma
17	3	12.0	9	1 LMT3 LOEMI	P41489 locusta mig
18	3	12.0	9	1 PKP1 PERAM	P82691 periplaneta
19	3	12.0	10	1 ANGT CHICK	P01018 gallus gall
20	3	12.0	10	1 GLEM HUMAN	P02728 homo sapien
21	3	12.0	10	1 LPK2 LOEMI	P41488 locusta mig
22	3	12.0	10	1 UPA4 HUMAN	P30090 homo sapien
23	3	12.0	11	1 CA42 LITCI	P82092 litoria cit
24	3	12.0	11	1 LPW TETH	P05624 thermus the
25	3	12.0	11	1 PKC1 CARMO	P82684 carausius m
26	3	12.0	12	1 LMT1 LOEMI	P22395 locusta mig
27	3	12.0	12	1 PKP4 PERAM	P82619 periplaneta
28	3	12.0	12	1 PKP4 PERU	P82690 periplaneta
29	3	12.0	13	1 UR2 FOLSP	P81022 polyodon sp
30	3	12.0	13	1 CXA2 CONGE	P01520 conus geogr
31	3	12.0	13	1 HPB9 RANES	P32416 rana esculi
32	3	12.0	13	1 LMT4 LOEMI	P41490 locusta mig
33	3	12.0	14	1 CAL1 CALGI	P20728 calotropis

34	3	12.0	14	1 LPW SALTY	P03054 salmonella
35	3	12.0	14	1 MAST PARID	P42716 parapolybia
36	3	12.0	14	1 MAST VESLE	P01514 vespa lew
37	3	12.0	14	1 MAST VESMA	P04205 vespa manda
38	3	12.0	14	1 MAST VESOR	P17238 vespa orien
39	3	12.0	14	1 MCRX METTM	P58315 methanobact
40	3	12.0	14	1 MY14 EISFO	P46979 eisenia foe
41	3	12.0	14	1 PPK6 PERAM	P82693 periplaneta
42	3	12.0	14	1 SMS MYOSC	P20750 myoxocephal
43	3	12.0	14	1 SMS ALLMI	P11885 alligator m
44	3	12.0	15	1 ASPI LACSN	P82648 lactobacilli
45	3	12.0	15	1 DIDH PSESP	P80701 pseudomonas
46	3	12.0	15	1 HSL1 PINPS	P81083 pinus pinas
47	3	12.0	15	1 SODM STRGR	P80733 streptomyce
48	3	12.0	16	1 CXA2 CONMA	P56636 conus magus
49	3	12.0	16	1 FIBA MUSVI	P14458 mustela vis
50	3	12.0	16	1 FOR1 MYRGU	P81438 myrmecia gu
51	3	12.0	16	1 FOR2 MYRGU	P81437 myrmecia gu
52	3	12.0	16	1 LPK1 LOEMI	P20404 locusta mig
53	3	12.0	16	1 RIPK TRIKI	P16093 trichosanthe
54	3	12.0	16	1 UVSX BPT6	Q06728 bacteriophage
55	3	12.0	16	1 YMOR PSEPU	Q02210 pseudomonas
56	3	12.0	17	1 APID BOMPA	P81464 bombus pasc
57	3	12.0	17	1 FLA2 BARBA	P35634 bartonella
58	3	12.0	17	1 MDH ACIDE	P80540 acidovorax
59	3	12.0	17	1 PPK5 PERAM	P82617 periplaneta
60	3	12.0	17	1 RM35 YEAST	P36530 saccharomyc
61	3	12.0	17	1 YALA TRYBB	P17961 trypanosoma
62	3	12.0	18	1 MU21 LITGE	P82068 litoria gen
63	3	12.0	18	1 PHPT PSESE	P25971 pseudaletia
64	3	12.0	19	1 MDH COMAC	P80539 comamonas a
65	3	12.0	19	1 MDH SHEON	P82177 shewanella
66	3	12.0	20	1 MDH KIBAR	P19978 kibdelospor
67	3	12.0	20	1 MDH MICGL	P19979 microtetras
68	3	12.0	20	1 PYR8 PYRAP	P37362 pyrrhocoris
69	3	12.0	20	1 SB18 MAIZE	P82967 zea mays (m
70	3	12.0	20	1 SODP PASPI	P81527 pasteurella
71	3	12.0	20	1 UN05 PINPS	P81674 pinus pinas
72	3	12.0	20	1 VMO2 CHICK	Q9P849 gallus gall
73	3	12.0	20	1 VSP1 TRIOK	P20005 trimeresaur
74	3	12.0	21	1 BOH1 BOWVA	P82282 bombina var
75	3	12.0	21	1 BOH4 BOWVA	P82284 bombina var

ALIGNMENTS

RESULT 1

ID	MISG MISAN	STANDARD	PRT	21 AA.
AC	P81474			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DE	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Misgurnin.			
OS	Misgurnus anguillicaudatus.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Cypriniformes;			
OC	Cobitidae; Misgurnus.			
OX	NCBI_TaxID=75329;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=97415401; PubMed=9271200;			
RA	Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;			
RT	"A novel antimicrobial peptide from the loach, Misgurnus			
RT	anguillicaudatus";			
RL	FEBS Lett. 411:173-178(1997).			
CC	-/- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL			
CC	GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.			
CC	-/- MASS SPECTROMETRY: MW=2502; METHOD=MALDI.			
KW	Antibiotic; Fungicide.			
SK	SEQUENCE 21 AA, 2502 MW; 4A6E9D0AB391BCF1 CRC64;			

Query Match 20.0%; Score 5; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
Db 12 KKGAA 16

RESULT 2

ID_FRA4_LITIN STANDARD; PRT; 24 AA.
AC P82023;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Frenatin 4.
OS Litoria infrafrenata (Giant tree frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Anura; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
the giant tree frog Litoria infrafrenata."
RL J. Pept. Sci. 2:117-124(1996).
CC -1- FUNCTION: WIDE SPECTRUM ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
GLANDS.
CC -1- MASS SPECTROMETRY: MW=2493; METHOD=FAB.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 24 AA; 2495 MW; 6986D063947805A1 CRC64;

Query Match 20.0%; Score 5; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 24
Db 6 LKKGAA 10

RESULT 3

ID_FJUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).
CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR; A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GAL...);
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5BLEBIE CRC64;

Query Match 16.0%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 EHS 17
Db 2 EHS 5

RESULT 4

ID_ATPB_CANFA STANDARD; PRT; 19 AA.
AC P99504;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
GN ATP5B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR HSC-2DPAGE; P99504; DOG.
DR InterPro; IPR00194; ATPase a/bcentre.
DR PROSITE; PS00152; ATPASE ALPHA BETA, PARTIAL.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolyase; ATP-binding;
KW Mitochondrion.
FT UNSURE 8
FT UNSURE 17 19
FT NON TER 19
SQ SEQUENCE 19 AA; 1871 MW; BB9C163FDC60BB42 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 25
Db 9 KGA 12

RESULT 5

ID_CYSP_TRIVA STANDARD; PRT; 22 AA.
AC P33404;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine proteinase (EC 3.4.22.-) (Fragment).
OS Trichomonas vaginalis.
OC Eukaryota; Parabasalidae; Trichomonadida; Trichomonadidae;
OC Trichomonadinae; Trichomonas.
OC NCBI_TaxID=5722;

RN SEQUENCE.
 RP MEDLINE=93307628; PubMed=8319888;
 RA Irvine J.W., Combs G.H., North M.J.,
 RT "Purification of cysteine proteinases from trichomonads using
 bacitracin-Sepharose.";
 RL FEMS Microbiol. Lett. 110:113-120(1993).
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR MEROPS; C01.082; -;
 DR InterPro; IPR000169; SHprot acsite.
 DR PROSITE; PS00139; THIOI PROTEASE CYS; PARTIAL.
 DR PROSITE; PS00639; THIOI PROTEASE HIS; PARTIAL.
 DR PROSITE; PS00640; THIOI PROTEASE ASN; PARTIAL.
 KW Hydrolase; Thiol protease.
 FT UNSURE 1
 FT NON_TER 22 22 OR K.
 SQ SEQUENCE 22 AA; 2398 MW; 0EE40FD86661ACCB CRC64;
 Query Match 16.0%; Score 4; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 KXGA 24
 DB 9 KXGA 12
 RESULT 6
 ALL5 HORSE
 ID ALL5 HORSE STANDARD; PRT; 23 AA.
 AC P82616;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dander allergen Equ c 5 (Fragments).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Hair dandruff;
 RX MEDLINE=21257838; PubMed=11358533;
 RA Goubard Botros H., Poncet P., Rabillon J., Fontaine T., Laval J.-M.,
 RA David B.,
 RT "Biochemical characterization and surfactant properties of horse
 allergens.";
 RT Allergens.";
 RL Eur. J. Biochem. 268:3126-3136(2001).
 CC -/- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -/- MASS SPECTROMETRY: MW=16700; METHOD=Electrospray.
 CC -/- MISCELLANEOUS: Allergen of horse dander. The determined pI of this
 protein is 5.25.
 KW Allergen.
 FT NON_TER 1 1
 FT NON_CONS 11 12
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2638 MW; 2406F19124582153 CRC64;
 Query Match 16.0%; Score 4; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPRL 8
 DB 9 LPRL 12
 RESULT 7
 FLA1 SULSH
 ID FLA1 SULSH STANDARD; PRT; 23 AA.
 AC Q9UWG6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 31/33 kDa flagellin (Fragment).
 OC Sulfolobus shibatae.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2286;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 51178 / DSM 5389 / B12;
 RX MEDLINE=96146545; PubMed=8550530;
 RA Faguy D.M., Bayley D.P., Kostyukova A.S., Thomas N.A., Jarrell K.F.;
 RT "Isolation and characterization of flagella and flagellin proteins
 from the Thermocacidophilic archaea Thermoplasma volcanium and
 Sulfolobus shibatae.";
 RL J. Bacteriol. 178:902-905(1996).
 CC -/- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
 FORM THE FILAMENTS OF FLAGELLA.
 CC -/- PFM: GLYCOSYLATED.
 CC -/- SIMILARITY: BELONGS TO THE ARCHAEAL FLAGELLIN FAMILY.
 KW Flagella; Glycoprotein.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2362 MW; BB372157B44DB3AC CRC64;
 Query Match 16.0%; Score 4; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 LIAP 11
 DB 10 LIAP 13
 RESULT 8
 RR19 PETHY
 ID RR19 PETHY STANDARD; PRT; 23 AA.
 AC P18550;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloroplast 30S ribosomal protein S19 (Fragment).
 GN RPS19.
 OS Petunia hybrida (Petunia).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
 OX NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89136067; PubMed=3224388;
 RA Aldrich J., Cherney B.W., Williams C., Merlin E.;
 RT "Sequence analysis of the junction of the large single copy region
 and the large inverted repeat in the petunia chloroplast genome.";
 RL Curr. Genet. 14:487-492(1988).
 CC -/- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
 to the 16S ribosomal RNA (By similarity).
 CC -/- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL; M37322; AAB02425.1;
 DR InterPro; IPR002222; Ribosomal_S19.
 DR Pfam; PF00203; Ribosomal_S19; I.
 DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
 KW Ribosomal protein; rRNA-binding; Chloroplast.
 FT INIT MET 0 0 BY SIMILARITY.
 FT NON_TER 23 23

SQ SEQUENCE 23 AA; 2665 MW; CA20D0128FC9AA49 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
|||
Db 3 SLKK 6

RESULT 9

PCWS_FACGO STANDARD; PRT; 24 AA.

AC P82427;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE "Ponerin W5.
OS achycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.

RC TISSUE=Venom;

RA MEDLINE=21264562; PubMed=11279030;
RX Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponerins, new antibacterial and insecticidal peptides from the
venom of the ant Pachycondyla goeldii."

RL J. Biol. Chem. 276:17823-17829(2001).

CC -1- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
AND GRAM-NEGATIVE BACTERIA AND S. CEREVISIAE. HAS INSECTICIDAL
CC AND HEMOLYTIC ACTIVITIES.

CC -1- MASS SPECTROMETRY: MW=2599.67; METHOD=WALDI.

CC Antibiotic; Insect immunity; Fungicide; Hemolysis.

QY SEQUENCE 24 AA; 2600 MW; DDEBEACAA7D1D7E CRC64;

Query Match 16.0%; Score 4; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGAA 25
|||
Db 7 KGAA 10

RESULT 10

CAD1_ENTFA STANDARD; PRT; 8 AA.

AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.

RA MEDLINE=85051889; PubMed=6437872;

RA Mori M., Sagami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.,
RT "Isolation and structure of the bacterial sex pheromone, cad1, that
induces plasmid transfer in Streptococcus faecalis."

RL FEBS Lett. 178:97-100(1984).

CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.

QY Pheromone.

QY SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
|||
Db 2 FSL 4

RESULT 11

LMT2_LOCFMI STANDARD; PRT; 8 AA.

AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyotropin 2 (LOM-MT-2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT cephalomyotropic peptide family."

RL Insect Biochem. 20:479-484(1990).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOTROPIC ACTIVITY).

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 8 AMIDATION.

SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
|||
Db 6 PRL 8

RESULT 12

LPK_LEUMA STANDARD; PRT; 8 AA.

AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Leukopyrokinin (LPK) (LEM-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoides; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.

RA MEDLINE=86269041; PubMed=3015140;

RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leukopyrokinin: structure-function studies."

RL Biochem. Biophys. Res. Commun. 137:936-942(1986).

CC [2]
CC -1- FUNCTION: AND SYNTHESIS.

QY SEQUENCE, AND SYNTHESIS.

QY TISSUE=Head;

QY MEDLINE=87052651; PubMed=2877794;

QY Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of a blocked myotropic
 RT neuropeptide isolated from the cockroach, Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
 CC PENTAPEPTIDE FRAGMENT FTPL.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR PIR; A23967.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9DSA1B6 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 6 PRL 8

RESULT 13
 ORMY_ORCLI STANDARD; PRT; 8 AA.
 AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orcomyotropin (OMT).
 OS Orcomyotropin (OMT) (spinycheek crayfish).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 CC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 CC Astacidea; Astacoidea; Cambaridae; Orconectes.
 OX NCBI_TaxID=28379;
 RN [1]

SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
 TISSUE=Hindgut;
 MEDLINE=20411310; PubMed=10952880;
 RA Dirksen H., Burdick S., Sauter A., Keller R.;
 RT "Two orcomyotins and the novel octapeptide orcomyotropin in the hindgut
 RT of the crayfish Orconectes limosus: identified myostimulatory
 RT neuropeptides originating together in neurons of the terminal
 RT abdominal ganglion.";
 RL J. Exp. Biol. 203:2807-2818(2000).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FA-
 CC Amidation; Neuropeptide.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 905 MW; 87661B1A9CDDA9 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 DB 3 APT 5

RESULT 14
 PPK2_PERAM STANDARD; PRT; 8 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach.";
 RL Peptides 18:473-478(1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 6 PRL 8

RESULT 15
 PPK3_PERAM STANDARD; PRT; 8 AA.
 AC P82678;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212459; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).

CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 6 PRL 8

RESULT 16
 CCAP CARMA STANDARD; PRT; 9 AA.
 AC 38556;
 DT J1-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cardioactive peptide (CCAP).
 OS Carcinus maenas (Common shore crab) (Green crab),
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 OS Tenebrio molitor (Yellow mealworm), and
 OS Spodoptera eridania (Southern armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759, 7130, 7067, 37547;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab Carcinus maenas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.sexta;
 RX MEDLINE=93050243; PubMed=1426284;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, Manduca sexta.";
 RL FEBS Lett. 313:165-168 (1992).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=8129851;
 RA Fuyua K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
 RA Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from Tenebrio
 RT molitor and Spodoptera eridania.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHROMOTROPIC.
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYPH.
 DR PIR; A26363; A26363.
 DR PIR; S27233; S27233.
 KW Neuropeptide; Amidation.
 FT DISULFID 3
 MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 959 MW; CSR861A9CDD44EB9 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 DB 5 APT 7

RESULT 17
 LMT3_LOCMI STANDARD; PRT; 9 AA.
 ID LMT3_LOCMI
 AC P41489;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamyotropin 3 (LOM-MT-3).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
 CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 7 PRL 9

RESULT 18
 PPK1_PERAM STANDARD; PRT; 9 AA.
 ID PPK1_PERAM
 AC P82691;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Pyrokinin-1 (Pea-PK-1) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT reticercbral complex of the American cockroach.";
 RL Peptides 18:473-478 (1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 DB 5 APT 7

CC -1- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; PYROKININ.
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 7 PRL 9

RESULT 19

ANGT_CHICK
 ID ANGT_CHICK STANDARD; PRT; 10 AA.
 AC F01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment).
 GN AGT OR SERPINAS.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.,
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.",
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]

RP SEQUENCE.
 RC SPECIES=C.C.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takei Y., Hasegawa Y.,
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.",
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II. THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A01250; A01250.
 DR PIR; A90917; A90917.
 DR PIR; A60624; A60624.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN, PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1232 MW; CEFBD761F2DB42 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 DB 8 FSL 10

RESULT 20

GLEM_HUMAN
 ID GLEM_HUMAN STANDARD; PRT; 10 AA.
 AC P02728;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythrocyte membrane glycopeptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72034940; PubMed=5286858;
 RA Weiss J.B., Lote C.J., Bobinski H.,
 RT "New low molecular weight glycopeptide containing triglycosylcysteine
 RT in human erythrocyte membrane.",
 RL Nature New Biol. 234:25-26(1971).
 CC -1- PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
 CC -1- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
 CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 CC ATTRIBUTED.
 DR PIR; A03187; XGHUE.
 KW Glycoprotein; Erythrocyte.
 FT CARBOHYD 1 1 S-LINKED (GLC...);
 SQ SEQUENCE 10 AA; 1049 MW; 239BFEEA1F5B18 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HSH 17
 DB 4 HSH 6

RESULT 21

LFK2_LOCOMI
 ID LFK2_LOCOMI STANDARD; PRT; 10 AA.
 AC P41488;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Psycoroptera; Orthoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94094539; PubMed=7903606;
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
 RA de Loof A.,
 RT "Isolation, identification and synthesis of locustapyrokinin II from
 RT Locusta migratoria, another member of the FXPRL-amide peptide
 RT family.",
 RL Comp. Biochem. Physiol. 106C:103-109(1993).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
 CC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAFA4271A9D1B772 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
Db 8 PRL 10

RESULT 22
ID UPA4 HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=9302937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.8. ITS MW IS: 40.5 kDa.
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TSE 14
Db 5 TSE 7

RESULT 23
ID CA42_LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Caerulein 4-2/4-2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz F.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
mountains tree frog Litoria citropa. Part 1. Sequence determination

RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- PTM: ISOFORM 4.2Y4 DIFFERS FROM ISOFORM 4.2 IN NOT BEING
SULFATED.
CC -1- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian skin; Hypotensive agent; Amidation; Sulfation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SHF 18
Db 7 SHF 9

RESULT 24
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRIPTOPHAN.

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CC -----
DR EMBL; X07744; CRA30565.1; --
DR PIR; S03315; LFTWWE
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
Db 2 ALP 4

RESULT 25
PKC1_CARNO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FAPRL-Amide).
 OS Carausius morosus (Indian stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;
 OC Heteronemidae; Carausius.
 OX NCBI_TaxID=7022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Predel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 insect, Carausius morosus (Phasmatodea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -|- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 11 11
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;

QY 6 PRL 8
 DB 9 PRL 11

RESULT 26
 LMT1_L0CMI STANDARD; PRT; 12 AA.
 ID LMT1_L0CMI
 AC P22395;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Locustamyotropin 1 (LOM-WT-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341077; PubMed=1974346;
 RA Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,
 RA Vandesande F., de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin
 (LOM-WT), a novel biologically active insect peptide.";
 RL Peptides 11:427-433(1990).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC FIR; A43975; A43975.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 12 12
 SQ SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 10 PRL 12

RESULT 27
 PPK4_PERAM STANDARD; PRT; 12 AA.
 ID PPK4_PERAM
 AC P82619;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 abdominal neurohemal organs of the American cockroach.";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 (MYOTROPIC ACTIVITY).
 CC -|- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -|- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 12 12
 SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAAL CRC64;

Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 10 PRL 12

RESULT 28
 PPK4_PERFU STANDARD; PRT; 12 AA.
 ID PPK4_PERFU
 AC P82630;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
 OS Periplaneta fuliginosa (Smokybrown cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=36977;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (-) MASS SPECTROMETRY: MW=1437.9; METHOD=WALDI.
 CC (-) SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; FALSE NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAA1 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 Db 10 PRL 12
 RESULT 29
 UR LSP STANDARD; PRT; 12 AA.
 ID UR2 POLSP STANDARD; PRT; 12 AA.
 AC P81022;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II (U-II) (UII).
 OS Polyodon spathula (North American paddlefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
 OC Polyodon.
 OX NCBI_TaxID=7913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spinal cord;
 RX MEDLINE=96051494; PubMed=8536944;
 RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
 RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
 RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
 RT spathula).";
 RL Gen. Comp. Endocrinol. 99:323-332(1995).
 CC (-) FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
 CC MUSCLE STIMULATION.
 CC (-) SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II; 1.
 DR PROSITE: PS00984; UROTENSIN_II; 1.
 KW ornone.
 FT ISULFID 6 11 BY SIMILARITY.
 SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 TSE 14
 Db 3 TSE 5
 RESULT 30
 CX22 CONGE STANDARD; PRT; 13 AA.
 ID CX2 CONGE STANDARD; PRT; 13 AA.
 AC F01520;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin GII.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN (1)

RP SEQUENCE.
 RX MEDLINE=81191854; PubMed=7014556;
 RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
 RT "Peptide toxins from Conus geographus venom.";
 RL J. Biol. Chem. 256:4734-4740(1981).
 RN (2)
 RP DISULFIDE BONDS.
 RX PubMed=6466616;
 RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
 RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
 RA Cruz L.J., Rivier J.;
 RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of
 RT iodinated derivatives.";
 RL Biochemistry 23:2796-2802(1984).
 CC (-) FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them.
 CC (-) SUBCELLULAR LOCATION: Secreted.
 CC (-) TISSUE SPECIFICITY: Expressed by the venom duct.
 CC (-) SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PIR; A01783; NTKN2G.
 DR HSPSP; P56973; I845.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 7
 FT DISULFID 3 13
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1422 MW; DDEE831C39297EBD CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 HFS 19
 Db 10 HFS 12
 RESULT 31
 HPB9 RANES STANDARD; PRT; 13 AA.
 ID HPB9 RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hemolytic protein B9 (Fragment).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8401;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90198965; PubMed=2317508;
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 RT extracts of Rana esculenta.";
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC (-) FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC (-) SUBCELLULAR LOCATION: Secreted.
 CC (-) TISSUE SPECIFICITY: SKIN.
 DR PIR; S09019; S09019.
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD_RES 13 13 AMIDATION.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIA 10
 DB 4 LIA 6

RESULT 32
 LMT4 LOCOMI
 ID LMT4 LOCOMI STANDARD; PRT; 13 AA.
 AC P41430;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustamytotropin 4 (LOM-MT-4).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota, Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamytotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamytotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
 CC STIMULATOR THAN LOM-MT I, II AND III.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ, 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 QY MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 DB 11 PRL 13

RESULT 33
 CALI CALGI
 ID CALI CALGI STANDARD; PRT; 14 AA.
 AC P20728;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calotropin DI (EC 3.4.22.-) (Fragment).
 OS Calotropis gigantea (Madag) (Bowstring hemp).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
 OC Asclepiadeae; Calotropis.
 OX NCBI_TaxID=4066;
 RN [1]
 RP SEQUENCE.
 RA Bhattacharya D., Sengupta A., Sinha N.K.;
 RA "Chemical modification and amino terminal sequence of calotropin DI
 RT from Calotropis gigantea.";
 RL Phytochemistry 26:633-636(1987).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR PIR; PT0026; PT0026.
 DR MEROPS; C01.011;
 DR InterPro; IPR000169; SHprot_abcite.
 DR PROSITE; PS00139; THIOL PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOL PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.

KW Hydrolase; Thiol protease.
 FT MOD_RES 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 24
 DB 11 KGA 13

RESULT 34
 LPW SALTY
 ID LPW SALTY STANDARD; PRT; 14 AA.
 AC P03054;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL OR TRPEE OR STM1722.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=78196931; PubMed=351195;
 RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
 RT "Comparison of the nucleotide sequences of the initial transcribed
 RT regions of the tryptophan operons of Escherichia coli and Salmonella
 RT typhimurium.";
 RL J. Mol. Biol. 121:193-217(1978).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.

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DR EMBL; M24960; -; NOT ANNOTATED_CDS.
 DR EMBL; AB008776; AAL20640.1; -;
 DR PIR; A03590; LPEBWT.
 DR StyGene; SG10400; trpl.
 KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
 DB 1 MAA 3

RESULT 35
 MAST PARID STANDARD; PRT; 14 AA.
 AC P42716; (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Mastoparan.
 OS Parapolybia indica.
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Polistinae; Parapolybia.
 OX NCBI_TaxID=31921;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Toki T., Yasuhara T., Nakajima T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 RT arapolybia indica."
 RL Jisei Dobutsu 39:105-111(1988).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR Mast cell degranulation; Venom; Amidation.
 KW MOD RES 14 14
 FT AMIDATION.
 SQ SEQUENCE 14 AA; 1619 MW; CA376CD3BA6D80DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
 |||
 DB 6 MAA 8

RESULT 36
 MAST VESLE STANDARD; PRT; 14 AA.
 AC P01514;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mastoparan.
 OS Vespa lewisii (Yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
 OX NCBI_TaxID=7452;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RA MEDLINE=80155337; PubMed=540362;
 RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
 RT "A new mast cell degranulating peptide 'mastoparan' in the venom of
 RT Vespa lewisii."
 RL Chem. Pharm. Bull. 27:1942-1944(1979).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR; A01776; QMWAVV.
 KW Mast cell degranulation; Venom; Amidation.
 FT MOD RES 14 14
 FT AMIDATION.
 SQ SEQUENCE 14 AA; 1480 MW; CC0C0EAC1D7B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
 |||
 DB 7 AAL 9

RESULT 37
 MAST VESMA STANDARD; PRT; 14 AA.
 AC P04205;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Mastoparan M (Mast cell-degranulating peptide).
 OS Vespa mandarinia (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7446;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
 RT "A new mast cell degranulating peptide, mastoparan-M, in the venom of
 RT the hornet Vespa mandarinia."
 RL Biomed. Res. 2:447-449(1981).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR; A01777; QMWMM.
 KW Mast cell degranulation; Venom; Amidation.
 FT MOD RES 14 14
 FT AMIDATION.
 SQ SEQUENCE 14 AA; 1480 MW; C85N7ECALD7B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
 |||
 DB 7 AAL 9

RESULT 38
 MAST VESOR STANDARD; PRT; 14 AA.
 AC P17238;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Mastoparan (Histamine releasing peptide I) (HR-I).
 OS Vespa orientalis (Oriental hornet).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pserygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7447;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
 RA Rozynov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 RT venom of Vespa orientalis hornet."
 RL Bioorg. Khim. 7:1467-1477(1981).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR; JN0389; JN0389.
 KW Mast cell degranulation; Venom; Amidation.
 FT MOD RES 14 14
 FT AMIDATION.
 SQ SEQUENCE 14 AA; 1494 MW; C84F9ECA026B00DD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
 |||
 DB 7 AAL 9

RESULT 39

MCRX METTM
ID MCRX METTM STANDARD; PRT; 14 AA.
AC P5815,
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.-.-) (MCR II alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
RT Rospert S., Linder D., Ellermann J., Thauer R.K.;
RA "Two genetically distinct methyl-coenzyme M reductases in Methanobacterium thermoautotrophicum strain Marburg and delta H."; Eur. J. Biochem. 194; 871-877 (1990).
RL Eur. J. Biochem. 194; 871-877 (1990).
CC -|- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)ethanesulfonic acid) with 7-mercaptoheptanoylthreonyl phosphate to methane and an heterodisulfide.
CC -|- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -|- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY) TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL PORPHINOID.
CC -|- PATHWAY: Methanogenesis; last step.
CC -|- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -|- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA. MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS CONTAINS MOSTLY MCR I.
KM Methanogenesis; Oxidoreductase; Multigene family.
FT NON-TER 14 14
SQ SEQUENCE 14 AA; 1718 MW; D317CCC562F00E29 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 LKX 22
DB 11 LKX 13

RESULT 40

MY14 EISFO
ID MY14 EISFO STANDARD; PRT; 14 AA.
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myosin active tetradecapeptide (ETP).
OS Eiseinia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Eiseinia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H., Nomoto K.;
RA "A novel gut tetradecapeptide isolated from the earthworm, Eiseinia foetida."; Peptides 16; 995-999 (1995).
RL Peptides 16; 995-999 (1995).
CC -|- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT MUSCLES.
CC -|- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 5 GAA 7

RESULT 41

PPKG PERAM
ID PPKG PERAM STANDARD; PRT; 14 AA.
AC P82693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-6 (Pea-PK-6) (FXPRK-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPRLamides in the nervous system of the American cockroach."; J. Comp. Neurol. 419; 352-363 (2000).
RL J. Comp. Neurol. 419; 352-363 (2000).
CC -|- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC -|- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN ABDOMINAL PERISYPHATHETIC ORGANS.
CC -|- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE PYROKINNIN FAMILY.
DR InterPro; IPR001484; Pyrokinnin.
KW Amidation; Pyrokinnin.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FP384A998 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
DB 12 PRL 14

RESULT 42

SMS1 MYOSC
ID SMS1 MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin), and Oncorhynchus kisutch (Coho salmon), and Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M. scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkmer S., Thim L.;
RT "Structural characterization of peptides derived from

RT prosomatostatins I and II isolated from the pancreatic islets of two
 RT species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 RN [2]

RP SEQUENCE
 RC SPECIES=O.kisutch, TISSUE=PANCREAS;
 RX MEDLINE=87055212; PubMed=2877919;
 RA Plietskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorman A.;
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
 RT somatostatins";
 RL Gen. Comp. Endocrinol. 63:252-263(1986).
 RN [3]

RP SEQUENCE
 RC SPECIES=A.anguilla; TISSUE=PANCREAS;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 RT structural features from the European eel (Anguilla anguilla).";
 RL Gen. Comp. Endocrinol. 72:181-189(1988).
 RN [1]

CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

DR PIR; S00172; S00172.

DR PIR; B60842; B60842.

DR PIR; A60840; A60840.

DR InterPro; IPR004250; Somatostatin.

DR Pfam; PF03002; Somatostatin; 1.

KW Hormone; Multigene family.

FT DISULFID 3 14

SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13

DB 11 FTS 13

RESULT 43

ID SMS_ALLMI STANDARD; PRT; 14 AA.

AC P31885;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-JUL-2001 (Rel. 40, Last annotation update)

DE somatostatin-14.

OS Alligator mississippiensis (American alligator), and

OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Crocodylidae; Alligatorinae; Alligator.

OX NCBI_TaxID=8496, 34903;

RN [1]

RP SEQUENCE.

RC SPECIES=A.mississippiensis; TISSUE=Stomach;

RX MEDLINE=93324451; PubMed=8101369;

RA Wang Y., Conlon J.M.;

RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain

RL and stomach of the alligator.";

RL Peptides 14:573-579(1993).
 RN [2]

RP SEQUENCE.

RC SPECIES=T. scripta; PubMed=1974347;

RX MEDLINE=90341082; PubMed=1974347;

RA Conlon J.M., Hicks J.W.;

RT "Isolation and structural characterization of insulin, glucagon and

RT somatostatin from the turtle, Pseudemys scripta.";

RL Peptides 11:461-466(1990).

CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.

DR PIR; C60414; C60414.

DR InterPro; IPR004250; Somatostatin.

DR Pfam; PF03002; Somatostatin; 1.

KW Hormone.

FT DISULFID 3 14 BY SIMILARITY.

SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13

DB 11 FTS 13

RESULT 44

ID ASPI_LACSN STANDARD; PRT; 15 AA.

AC P82648;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Acid shock protein 1 (Fragment).

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=1625;

RN [1]

RP SEQUENCE.

RC STRAIN=CB1;

RX MEDLINE=21322712; PubMed=11429463;

RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;

RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";

RL Microbiology 147:1863-1873(2001).

CC -!- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 12.0%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 23

DB 3 KKG 5

RESULT 45

ID DIDH_PSESP STANDARD; PRT; 15 AA.

AC P80701;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE 3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)

OS Pseudomonas sp.

OC Bacteria; Proteobacteria.

OX NCBI_TaxID=306;

RN [1]

RP SEQUENCE.

RX MEDLINE=97100200; PubMed=8944761;

RA Oppermann U.C.T., Maser E.;

RT "Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl

reductase from the Gram-negative bacterium Comamonas testosteroni.";

RL Eur. J. Biochem. 241:744-749(1996).

CC -!- FUNCTION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND

3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED

A/B RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL

COMPOUNDS, INCLUDING A METHYRONE-BASED CLASS OF INSECTICIDES, TO

THE RESPECTIVE ALCOHOL METABOLITES.

CC -!- CATALYTIC ACTIVITY: Androstosterone + NAD(P)(+) = 5-alpha-androstane-

3.17-dione + NAD(P)H.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
 CC InterPro: IPR002198; ADH short.
 CC PROSITE: PS00061; ADH_SHORT, PARTIAL.
 KW Oxidoreductase; NAD.
 FT DOMAIN 6 >15 INVOLVED IN COFACTOR BINDING
 FT (BY SIMILARITY).
 FT NON TER 15 15
 FT SEQUENCE 15 AA; 1315 MW; 9506860D070AY790 CRC64;
 SQ
 Query Match 12.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 GAA 25
 DB 13 GAA 15
 RESULT 46
 HS11 PINPS STANDARD; PRT; 15 AA.
 AC P81083;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable class I heat shock protein (Water stress responsive protein
 DE 3) (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 CC NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RP TISSUE=Needle;
 RX MEDLINE=9418576; PubMed=9747804;
 RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
 RA "Water-deficit-responsive proteins in maritime pine."
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RP TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RA "Separation and characterization of needle and xylem maritime pine
 RA proteins."
 RL Electrophoresis 20:1098-1108(1999).
 RN [3]
 RP REVISION TO 1.
 RA Frigerio J.-M.;
 RL Submitted (SEP-2001) to the SWISS-PROT data bank.
 CC -1- SUBUNIT: FORMS OLIGOMERIC STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- INDUCTION: BY WATER STRESS.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
 CC (SPOT N144) IS: 6.1, ITS MW IS: 17 kDa.
 CC -1- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
 CC FAMILY.
 CC -1- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
 CC WHICH ARE CYTOPLASMIC, CLASS III WHICH IS IN THE CHLOROPLAST
 CC AND CLASS IV WHICH IS IN THE ENOMEMERANE. THIS PROTEIN BELONGS
 CC TO CLASS I.
 CC InterPro: IPR002068; Hsp20.
 DR PROSITE: PS01031; HSP20, PARTIAL.
 KW Heat shock; Multigene family.
 FT NON TER 1 15
 FT SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;
 SQ
 Query Match 12.0%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 FSL 20
 DB 5 FSL 7
 RESULT 47
 SODM_STRGR STANDARD; PRT; 15 AA.
 ID SODM_STRGR
 AC P80733;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
 GN SOD2.
 OS Streptomyces griseus.
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 CC NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE.
 RP STRAIN=KCTC 9006;
 RX MEDLINE=97056064; PubMed=8900409;
 RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
 RA Kang S.-O.;
 RA "Unique isozymes of superoxide dismutase in Streptomyces griseus."
 RL Arch. Biochem. Biophys. 334:341-348(1996).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Iron and zinc.
 CC -1- SUBUNIT: Tetramer.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; Sodfe; 1.
 DR PROSITE: PS00088; SOD MN; PARTIAL.
 KW Oxidoreductase; Iron; Zinc.
 FT NON TER 15 15
 FT SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;
 SQ
 Query Match 12.0%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AAL 5
 DB 13 AAL 15
 RESULT 48
 CXA2_CONMA STANDARD; PRT; 16 AA.
 ID CXA2_CONMA
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 CC NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=96205934; PubMed=8631783;
 RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 RA McIntosh J.M.;
 RA "A new alpha-conotoxin which targets alpha3beta2 nicotinic
 RA acetylcholine receptors."
 RL J. Biol. Chem. 271:7522-7528(1996).

[2]
RP STRUCTURE BY NMR.
RA MEDLINE=98062282; PubMed=9398298;
RX Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
RT "three-dimensional solution structure of alpha-conotoxin MII, an
RT alpha/beta2 neuronal nicotinic acetylcholine receptor-targeted
RT ligand.";
RL Biochemistry 36:15693-15700(1997).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99060038; PubMed=9843366;
RA Hill J.M., Omen C.J., Miranda L.P., Bingham J.P., Alewood P.F.,
RA Craik D.J.;
RT "three-dimensional solution structure of alpha-conotoxin MII by NMR
RT spectroscopy: effects of solution environment on helicity.";
RL Biochemistry 37:15621-15630(1998).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
CC NACHR SUBUNIT COMBINATIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PDB; 1MII; 21-OCT-98.
DR PDB; 1M2C; 13-JAN-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD RES 16 16
FT SEQUENCE 16 AA; 1716 MW; 2822AF190166CAF9 CRC64;
SQ
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 EHS 16
DB 11 EHS 13
RESULT 49
FIBRINOPEPTIDE A.
ID FIBRINOPEPTIDE A. PRT; 16 AA.
AC P14458.
DT 1-JAN-1990 (Rel. 13, Created)
DT 31-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA) LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW

FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 GAA 25
DB 12 GAA 14
RESULT 50
FOR2 MYRGU
ID FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81438;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Formaein 1.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Myrmecinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RX TISSUE=Hemolymph; PubMed=9497332;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides.";
RL J. Biol. Chem. 273:6139-6143(1998).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E. COLI
CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC BACTERIA.
CC -1- INDUCTION: By bacterial infection.
CC -1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -1- SIMILARITY: TO DROSOPHILA DROSOCIN.
KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
FT CARBOHYD 11 11 O-LINKED (GALNAC...);
FT SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;
SQ
Query Match 12.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PRL 8
DB 14 PRL 16
RESULT 51
FOR2 MYRGU
ID FOR2 MYRGU STANDARD; PRT; 16 AA.
AC P81437;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Formaein 2.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Formicidae; Myrmecinae; Myrmecia.
OX NCBI_TaxID=36170;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RX TISSUE=Hemolymph;
RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible

RT O-glycosylated proline-rich antibacterial peptides.";
 RL J. Biol. Chem. 273:6139-6143(1998).
 CC -|- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E. COLI
 CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
 CC BACTERIA.
 CC -|- INDUCTION: By bacterial infection.
 CC -|- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAc DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -|- SIMILARITY: TO DROSOPHILA DROSOCIN.
 CC Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 KW CARBOHYD 11 O-LINKED (GALNAc...)
 FT SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;
 SQ
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 Db 14 PRL 16
 RESULT 52
 LPK1 LOCM1 STANDARD; PRT; 16 AA.
 AC P20404;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustapyrokinin 1 (LOM-PK-1).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Prorygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 CC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
 RT myotropic peptide of Locusta migratoria."
 RL Gen. Comp. Endocrinol. 81:97-104(1991).
 CC -|- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 CC PIR; A49761; A49761.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRL 8
 Db 14 PRL 16
 RESULT 53
 RIPK TRIKI STANDARD; PRT; 16 AA.
 ID RIPK TRIKI
 AC P1603;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein trichokirin (rRNA N-glycosidase)
 DE (EC 3.2.2.22) (Fragment).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eusoids 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=89005108; PubMed=3262509;
 RA Casellas P., Dussosoy D., Falasca A.I., Barbieri L., Stirpe F.;
 RA Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F.;
 RT trichokirin, a ribosome-inactivating protein from the seeds of
 RT Trichosanthes kirilowii Maximowicz. Purification, partial
 RT characterization and use for preparation of immunotoxins."
 RL Eur. J. Biochem. 176:581-588(1988).
 CC -|- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -|- PTM: GLYCOSYLATED.
 CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC PIR; S01669; S01669.
 DR InterPro; IPR001574; RIP.
 DR PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
 KW Glycoprotein.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1605 MW; 5E268A7F345935A2 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 FSL 20
 Db 4 FSL 6
 RESULT 54
 UVSX BPT6 STANDARD; PRT; 16 AA.
 ID UVSX BPT6
 AC Q06728;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Recombination and repair protein (Fragment).
 CC UVSX
 GN Bacteriophage T6.
 OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OX NCBI_TaxID=10666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219141; PubMed=8464751;
 RA Winkler M., Rueger W.;
 RT "Cloning and sequencing of the genes of
 RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2
 RT and T6."
 RL Nucleic Acids Res. 21:1500-1500(1993).
 CC -|- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND
 CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.
 CC INTERACTS WITH DDA AND GENE 32 PROTEINS.
 CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC EMBL; X68725; CAA48668.1; -.
 DR PIR; S35627; S35627.
 KW DNA damage; DNA replication; DNA recombination; DNA repair;

KW ATP-binding. 16
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLI 9
 Db 9 RLI 11

RESULT 55
 YNOR_PSEPU STANDARD; PRT; 16 AA.
 ID YNOR_PSEPU
 AC Q02210;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 06-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in MORA 3 region (Fragment).
 OS Pseudomonas putida.
 OG Plasmid pMDH7.2.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M10;
 RX MEDLINE=93119531; PubMed=8452544;
 RA Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.;
 RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a
 RL plasmid-encoded gene from Pseudomonas putida M10.";
 RL Biochem. J. 290:539-544(1993).
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 CC -----
 DR EMBL; M94775; AAB17357.1; -.
 DR PIR; S30384; S30384.
 KW Hypothetical protein; Plasmid.
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;
 Query Match 12.0%; Score 3; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LPR 7
 Db 6 LPR 8

Search completed: December 19, 2002, 17:42:25
 Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 ; Search time 28 Seconds
(without alignments)
183.971 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GWAALPRLIAPTSEHSFLKKGAA 25

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database :

SPTEMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_nhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	6	24.0	10	5 QSWPE7	Qswpe7 skogsbergia
2	5	20.0	24	8 QSHG7	Qshg7 chamaeleo h
3	5	20.0	25	11 Q63999	Q63999 rattus sp.
4	5	20.0	25	11 Q64000	Q64000 rattus sp.
5	5	20.0	25	16 Q26056	Q26056 helicobacte
6	4	16.0	6	10 P82541	P82541 spinacia ol
7	4	16.0	8	2 Q56429	Q56429 thermus the
8	4	16.0	8	8 Q36898	Q36898 nicotiana p
9	4	16.0	9	5 Q9VV82	Q9VV82 drosophila
10	4	16.0	10	12 Q90347	Q90347 hepatitis g
11	4	16.0	12	10 P94011	P94011 arabidopsis
12	4	16.0	13	8 Q33417	Q33417 digitalis p
13	4	16.0	15	8 Q37016	Q37016 nicotiana a
14	4	16.0	16	8 Q36789	Q36789 solanum nig
15	4	16.0	18	4 Q16167	Q16167 homo sapien
16	4	16.0	18	5 Q26833	Q26833 trypanosoma

17	4	16.0	19	2 Q9R4A3	Q9r4a3 escherichia
18	4	16.0	19	3 Q9UR87	Q9ur87 candida par
19	4	16.0	19	4 Q9UCE4	Q9uce4 homo sapien
20	4	16.0	19	8 Q36925	Q36925 nicotiana v
21	4	16.0	20	1 Q9UWJ2	Q9uwj2 methanospir
22	4	16.0	20	8 Q36584	Q36584 nicotiana g
23	4	16.0	20	8 Q36806	Q36806 solanum tub
24	4	16.0	24	8 Q8SK10	Q8sk10 furcifer ca
25	4	16.0	24	8 Q8SHJ1	Q8shj1 chamaeleo c
26	4	16.0	24	8 Q8SH18	Q8sh18 chamaeleo c
27	4	16.0	24	8 Q8SHA7	Q8sha7 brookesia a
28	4	16.0	24	8 Q8SHA4	Q8sha4 brookesia b
29	4	16.0	24	8 Q8SH98	Q8sh98 brookesia p
30	4	16.0	24	8 Q8SH95	Q8sh95 brookesia p
31	4	16.0	24	8 Q8SH92	Q8sh92 brookesia s
32	4	16.0	24	8 Q8SH89	Q8sh89 brookesia t
33	4	16.0	24	8 Q8SH87	Q8sh87 brookesia t
34	4	16.0	24	8 Q8SH84	Q8sh84 brookesia t
35	4	16.0	24	10 Q9AUE9	Q9aue9 brassica na
36	4	16.0	24	13 P82833	P82833 rana berla
37	4	16.0	24	13 P82834	P82834 rana berla
38	4	16.0	24	13 P82838	P82838 rana berla
39	4	16.0	25	4 Q96F56	Q96f56 homo sapien
40	4	16.0	25	15 Q85452	Q85452 moloney mur
41	3	12.0	7	12 Q66113	Q66113 cherry leaf
42	3	12.0	8	2 O09258	O09258 synechococc
43	3	12.0	8	2 Q9AGP4	Q9agp4 arthrobacte
44	3	12.0	8	3 P82858	P82858 puccinia re
45	3	12.0	8	11 Q9ERD2	Q9erd2 mus musculu
46	3	12.0	8	11 Q9QVK5	Q9qvk5 rattus sp.
47	3	12.0	9	2 Q9R7H9	Q9r7h9 haemophilus
48	3	12.0	9	4 Q14277	Q14277 homo sapien
49	3	12.0	9	5 Q9TWV0	Q9twv0 anthopleura
50	3	12.0	9	6 Q9TRW2	Q9trw2 oryctolagus
51	3	12.0	9	10 Q988J8	Q988j8 oryza sativ
52	3	12.0	9	11 Q88889	Q88889 mus musculu
53	3	12.0	9	12 Q90350	Q90350 hepatitis g
54	3	12.0	9	12 Q9E1U7	Q9e1u7 hepatitis b
55	3	12.0	10	2 Q9X533	Q9x533 escherichia
56	3	12.0	10	2 Q9X534	Q9x534 leclercia a
57	3	12.0	10	2 Q9F5W1	Q9f5w1 vibrio chol
58	3	12.0	10	2 Q9AE19	Q9ae19 streptococc
59	3	12.0	10	2 Q60194	Q60194 spiroplasma
60	3	12.0	10	2 P83154	P83154 anabaena sp
61	3	12.0	10	3 Q8TG88	Q8tg88 pleurotus o
62	3	12.0	10	4 Q9H3R9	Q9h3r9 homo sapien
63	3	12.0	10	8 Q9T2P3	Q9t2p3 rattus sp.
64	3	12.0	10	8 Q8SHP0	Q8shp0 bradypodion
65	3	12.0	10	8 Q8SHM2	Q8shm2 calumma boe
66	3	12.0	10	8 Q8SHL3	Q8shl3 calumma fur
67	3	12.0	10	8 Q8SHL0	Q8shl0 calumma gas
68	3	12.0	10	8 Q8SHK1	Q8shk1 calumma nas
69	3	12.0	10	10 Q41788	Q41788 zea mays (m
70	3	12.0	10	11 Q9QVK8	Q9qvk8 mus sp. mep
71	3	12.0	10	12 P90373	P90373 pseudorabie
72	3	12.0	10	15 Q75595	Q75595 human immun
73	3	12.0	11	2 Q9S618	Q9s618 prochloroco
74	3	12.0	11	2 Q47451	Q47451 escherichia
75	3	12.0	11	2 P77404	P77404 escherichia

ALIGNMENTS

RESULT 1	QSWPE7	PRELIMINARY;	PRT;	10 AA.
QSWPE7	QSWPE7			
ID	QSWPE7			
AC	QSWPE7			
DT	01-MAR-2002 (T-EMBLrel. 20, Created)			
DT	01-MAR-2002 (T-EMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (T-EMBLrel. 20, Last annotation update)			
DE	Open (Fragment).			
OS	Skogsbergia lernerii.			

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Ostracoda; Myodocopa;
 OX Myodocopa; Cypridinoida; Cypridinidae; Skogsbergia.
 RN [1]_TaxID=176979;
 RP SEQUENCE FROM N.A.
 RC TISSUE-ENTIRE ORGANISM;
 RA Oakley T.H., Huber D.R.;
 RT "Eye-specific expression of multiple opsin loci in ostracod
 crustaceans";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF353377; AAL37547.1; --
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1035 MW; 1F4B3117672DDDD4 CRC64;
 Query Match 24.0%; Score 6; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.4; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 3 AALPRL 8
 DB 4 AALPRL 9
 RESULT 2
 Q63999
 ID Q63999 PRELIMINARY; PRT; 24 AA.
 AC Q63999
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN ND1.
 OS Chamaeleo hoehnelti.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylia; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
 OX NCBI_TaxID=179913;
 RN [1]_TaxID=179913;
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448752; AAL90536.1; --
 FT NON_TER 1
 SQ SEQUENCE 24 AA; 2638 MW; A253FFAE30A281CA CRC64;
 Query Match 20.0%; Score 5; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 2 MAALP 6
 DB 20 MAALP 24
 RESULT 3
 Q63999
 ID Q63999 PRELIMINARY; PRT; 25 AA.
 AC Q63999
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Vasopressin (Fragment).
 GN VASOPRESSIN, VP.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]_TaxID=10118;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94286576; PubMed=8016115;

RA Evans D.A., van der Kleij A.A., Sonnemans M.A., Burbach J.P.,
 RA van Leeuwen F.W.;
 RT "Frameshift mutations at two hotspots in vasopressin transcripts in
 post-mitotic neurons";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063 (1994).
 DR EMBL; S71426; AAB31127.1; --
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2478 MW; 4D78687ACF623B59 CRC64;
 Query Match 20.0%; Score 5; DB 11; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 3 AALPR 7
 DB 4 AALPR 8
 RESULT 4
 Q64000
 ID Q64000 PRELIMINARY; PRT; 25 AA.
 AC Q64000
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Vasopressin (Fragment).
 GN VASOPRESSIN, VP.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]_TaxID=10118;
 RP SEQUENCE FROM N.A.
 RA Evans D.A., van der Kleij A.A., Sonnemans M.A., Burbach J.P.,
 RA van Leeuwen F.W.;
 RT "Frameshift mutations at two hotspots in vasopressin transcripts in
 post-mitotic neurons";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:6059-6063 (1994).
 DR EMBL; S71427; AAB31128.1; --
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2455 MW; B1F1B5E4D310F237 CRC64;
 Query Match 20.0%; Score 5; DB 11; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;
 QY 3 AALPR 7
 DB 4 AALPR 8
 RESULT 5
 Q26056
 ID Q26056 PRELIMINARY; PRT; 25 AA.
 AC Q26056
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
 DE Hypothetical protein HP1528.
 GN HP1528.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]_TaxID=210;
 RP SEQUENCE FROM N.A.
 RA STRAIN=26695 / ATCC 700392;
 RC MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter pylori*.";
 RL Nature 388:539-547 (1997).
 DR EMBL; AEO00651; RAD08577.1; --
 DR TIGR; HPI528; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 25 AA; 3075 MW; 508093A41CE396E CRC64;
 Query Match 20.0%; Score 5; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 SLKKG 23
 DB 13 SLKKG 17
 RESULT 6
 P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE Chloroplast 308 ribosomal protein S19 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=33562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465 (2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 FORM IS THE MINOR BASIC FORM.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR002222; Ribosomal S19.
 DR Pfam; PF00203; Ribosomal S19; PARTIAL.
 DR PRINTS; PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER
 SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 16.0%; Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKKG 22
 DB 3 SLKKG 6

RESULT 7
 Q56429 PRELIMINARY; PRT; 8 AA.
 ID Q56429

AC Q56429;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE GAPDH (Fragment).
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB-8;
 RX MEDLINE=89025722; PubMed=3052437;
 RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
 RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
 extreme thermophile, *Thermus thermophilus*.";
 RL Biochem. J. 254:509-517 (1988).
 DR EMBL; X12464; CAA31005.1; --
 FT NON TER
 SQ SEQUENCE 8 AA; 885 MW; 33C87333732C72B CRC64;

Query Match 16.0%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKG 23
 DB 4 LKKG 7

RESULT 8
 Q36898 PRELIMINARY; PRT; 8 AA.
 AC Q36898;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE RPS19; protein (Fragment).
 GN RPS19;
 OS Nicotiana glauca, and
 OS Nicotiana glauca (Bigelow's tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=49453; 4088;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RL Mol. Gen. Genet. 0:0-0 (1996).
 DR EMBL; Z71234; CAA94933.1; --
 DR ENBL; Z71225; CAA94921.1; --
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 8 AA; 977 MW; FD43333735A411A6 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKKG 22
 DB 4 SLKKG 7

RESULT 9
 Q9VV82 PRELIMINARY; PRT; 9 AA.
 AC Q9VV82;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)
 DE CG18219 protein (Fragment).


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KW Chloroplast. 13
FT NON TER 13
SQ SEQUENCE 13 AA, 1518 MW, 4D775A09A5SD4333 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 13
Q37016 PRELIMINARY; PRT; 15 AA.
ID Q37016
AC Q37016;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19.
OS Nicotiana glauca (Winged tobacco) (Persian tobacco),
OS Nicotiana glauca (Common tobacco), and
OS Nicotiana glutinosa (Tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4087, 4097, 35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL Mol. Gen. Genet. 0:0-0(1996).
DR EMBL; Z71239; CAA94944.1; -
DR EMBL; Z71236; CAA94937.1; -
DR EMBL; Z71238; CAA94942.1; -
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast. 15
FT NON TER 15
SQ SEQUENCE 15 AA, 1756 MW, 09DE1D775A138C5D CRC64;

Query Match 16.0%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 14
Q36789 PRELIMINARY; PRT; 16 AA.
ID Q36789
AC Q36789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Rps19, protein (Fragment).
GN Rps19.
OS Solanum nigrum (Black nightshade).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4112;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL "Ebb and Flow of the Chloroplast Inverted Repeat.";
Mol. Gen. Genet. 252:195-206(1996).

KW Chloroplast. 13
FT NON TER 13
SQ SEQUENCE 13 AA, 1518 MW, 4D775A09A5SD4333 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 13
Q37016 PRELIMINARY; PRT; 15 AA.
ID Q37016
AC Q37016;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19.
OS Nicotiana glauca (Winged tobacco) (Persian tobacco),
OS Nicotiana glauca (Common tobacco), and
OS Nicotiana glutinosa (Tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4087, 4097, 35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL Mol. Gen. Genet. 0:0-0(1996).
DR EMBL; Z71239; CAA94944.1; -
DR EMBL; Z71236; CAA94937.1; -
DR EMBL; Z71238; CAA94942.1; -
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast. 15
FT NON TER 15
SQ SEQUENCE 15 AA, 1756 MW, 09DE1D775A138C5D CRC64;

Query Match 16.0%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 14
Q36789 PRELIMINARY; PRT; 16 AA.
ID Q36789
AC Q36789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Rps19, protein (Fragment).
GN Rps19.
OS Solanum nigrum (Black nightshade).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4112;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL "Ebb and Flow of the Chloroplast Inverted Repeat.";
Mol. Gen. Genet. 252:195-206(1996).

KW Chloroplast. 16
FT NON TER 16
SQ SEQUENCE 16 AA, 1869 MW, 1AB9DE1D775A138C CRC64;

Query Match 16.0%; Score 4; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 15
Q16167 PRELIMINARY; PRT; 18 AA.
ID Q16167
AC Q16167;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Serum albumin (Fragment).
GN SERUM ALBUMIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Madlison J., Galliano M., Watkins S., Minchiotti L., Porta F.,
RA Rossi A., Putnam F.W.;
RT "Genetic variants of human serum albumin in Italy: point mutants and a
RT carboxyl-terminal variant.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).
DR EMBL; S70799; AAB31177.1; -
FT NON TER 1
SQ SEQUENCE 18 AA, 2089 MW, 2CCF6C5B0B08690B CRC64;

Query Match 16.0%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALPR 7
Db 3 ALPR 6

RESULT 16
Q26833 PRELIMINARY; PRT; 18 AA.
ID Q26833
AC Q26833;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Iafat 1.2) variant surface glycoprotein BC gene (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown K.H., Brentano S.T., Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA.";
RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14021; AAA30306.1; -
FT NON TER 1
SQ SEQUENCE 18 AA, 2039 MW, 8EA0F51BD630BF8F CRC64;

Query Match 16.0%; Score 4; DB 5; Length 18;

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Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LIAP 11
DB 11 LIAP 14

RESULT 17
Q9R4A3 PRELIMINARY; PRT; 19 AA.
AC Q9R4A3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE N-acetyl-D-NEURAMINIC acid lyase (EC 4.1.3.3) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX 'CBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96276413; PubMed=9694758;
RA Ferrero M.A., Reglero A., Fernandez-Lopez M., Ordas R.,
RA Rodriguez-Aparicio L.B.;
RT "N-acetyl-D-neuraminic acid lyase generates the sialic acid for
RT colominic acid biosynthesis in Escherichia coli K1."
RL Biochem. J. 317:157-165 (1996).
SQ SEQUENCE 19 AA; 2061 MW; 72022247A20EBBE3 CRC64;

Query Match 16.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
DB 8 MAAL 11

RESULT 18
Q9UR87 PRELIMINARY; PRT; 19 AA.
AC Q9UR87;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Class I cytochrome C isoform B (Fragment).
OS Candida parapsilosis (Yeast).
OC Ascomycota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX 'CBI_TaxID=5480;
RN [1]
RP SEQUENCE.
RX MEDLINE=93305688; PubMed=8391313;
RA Camougrand N., Velours J., Denis M., Guerin M.;
RT "Isolation, characterization and function of the two cytochromes c of
RT the yeast Candida parapsilosis."
RL Biochim. Biophys. Acta 1143:135-141 (1993).
SQ SEQUENCE 19 AA; 2108 MW; 17023D754PF25F87 CRC64;

Query Match 16.0%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
DB 10 KKGA 13

RESULT 19
Q9UCE4 PRELIMINARY; PRT; 19 AA.
ID Q9UCE4
AC Q9UCE4;

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DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE PROCATHEPSIN E (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX 'NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93349047; PubMed=8346912;
RA Takeda-Ezaki M., Yamamoto K.;
RT "Isolation and biochemical characterization of procathepsin E from
RT human erythrocyte membranes."
RL Arch. Biochem. Biophys. 304:352-358 (1993).
SQ SEQUENCE 19 AA; 2293 MW; 3217ABB8670A65FC CRC64;

Query Match 16.0%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 12 SLKK 15

RESULT 20
Q36925 PRELIMINARY; PRT; 19 AA.
AC Q36925;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE RPS19, protein (Fragment).
GN RPS19;
OS Nicotiana velutina,
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco), and
OS Nicotiana attenuata.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX 'NCBI_TaxID=49454; 4092, 49451;
RN [1]
RP SEQUENCE FROM N.A.
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RL Mol. Gen. Genet. 0:0-0 (1996).
DR EMBL; Z71240; CAA94946.1; -
DR EMBL; Z71242; CAA94950.1; -
DR EMBL; Z71243; CAA94952.1; -
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; I.
KW Chloroplast.
FT NON TER
RP SEQUENCE 19 AA; 2239 MW; 19AA300AB9DE1D77 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 4 SLKK 7

RESULT 21
Q9UWJ2 PRELIMINARY; PRT; 20 AA.
ID Q9UWJ2
AC Q9UWJ2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE 35 kDa flagellin (Fragment).

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OS Methanospirillum hungatei.
OC Archaea; Euryarchaeota; Methanococci; Methanomicrobiales;
OC Methanomicrobiaceae; Methanospirillum.
OX NCBI_TaxID=2203;
RN [1]
RP SEQUENCE.
RX MEDLINE=95095917; PubMed=8002572;
RA Faguy D.M., Koval S.F., Jarell K.F.;
RT "Physical characterization of the flagella and flagellins from
RT Methanospirillum hungatei.",
RL J. Bacteriol. 176:17491-7498 (1994).
SQ SEQUENCE 20 AA; 2036 MW; B2244BC7818F8799 CRC64;

Query Match 16.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 8 LIAP 11
Db 10 LIAP 13

RESULT 22
Q36584 PRELIMINARY; PRT; 20 AA.
ID Q36584
AC Q36584;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Rps19' protein (Fragment).
GN RPS19'.
OS Nicotiana glauca (Glaucous tobacco) (Tree tobacco).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanales.
OX NCBI_TaxID=4090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UNIV. OF BIRMINGHAM;
RX MEDLINE=96397499; PubMed=8804393;
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.",
RL Mol. Gen. Genet. 252:195-206(1996).
DR EMBL; Z71244; CAA94954.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast.
FT NON TER 20
SQ SEQUENCE 20 AA; 2398 MW; 2FC9AA300459DE1D CRC64;

Query Match 16.0%; Score 4; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 23
Q36806 PRELIMINARY; PRT; 23 AA.
ID Q36806
AC Q36806;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Rps19' protein (Fragment).
GN RPS19'.
OS Solanum tuberosum (Potato).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96397499; PubMed=8804393;
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
RT "Ebb and Flow of the Chloroplast Inverted Repeat.",
RL Mol. Gen. Genet. 252:195-206(1996).
DR EMBL; Z71247; CAA94960.1; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
KW Chloroplast.
FT NON TER 23
SQ SEQUENCE 23 AA; 2709 MW; 9DD0128FC9AA300A CRC64;

Query Match 16.0%; Score 4; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 SLKK 22
Db 4 SLKK 7

RESULT 24
Q8SK10 PRELIMINARY; PRT; 24 AA.
ID Q8SK10
AC Q8SK10;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Furfifer campani.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Chamaeleonidae; Furfifer.
OX NCBI_TaxID=179925;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).",
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF48766; AAL90578.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2588 MW; C95A0D19C55B81CB CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 AALP 6
Db 21 AALP 24

RESULT 25
Q8SHJ1 PRELIMINARY; PRT; 24 AA.
ID Q8SHJ1
AC Q8SHJ1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Chamaeleo calyptratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=179908;
RN [1]

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RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448774; AAL90512.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2664 MW; A61DC2AE354791CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
DB 21 AALP 24

RE 26
Q8 SHI8 PRELIMINARY; PRT; 24 AA.
AC Q8SHI8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Chamaeleo chamaeleon.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=91907;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448745; AAL90515.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2662 MW; B81C3D8D20F791CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
DB 21 AALP 24

RESULT 27
Q8SH7 PRELIMINARY; PRT; 24 AA.
ID Q8SH7;
AC Q8SH7;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Brookesia antioetreae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179891;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF448773; AAL90599.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2652 MW; BD082475311691CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
DB 21 AALP 24

RESULT 28
Q8SH4 PRELIMINARY; PRT; 24 AA.
ID Q8SH4;
AC Q8SH4;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Brookesia brygool.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179892;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448774; AAL90602.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2596 MW; A22A1975310AEF2A CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
DB 21 AALP 24

RESULT 29
Q8SH9 PRELIMINARY; PRT; 24 AA.
ID Q8SH9;
AC Q8SH9;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN ND1.
OS Brookesia perarmata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179894;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448776; AAL90608.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2652 MW; BD1701D6310AEF2A CRC64;

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Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 30

Q8SH95 PRELIMINARY; PRT; 24 AA.
 AC Q8SH95;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia peyeriasi.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=91904;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448777; AAL90611.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2654 MW; 9AF827BA3DF8A4D5 CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 31

Q8SH92 PRELIMINARY; PRT; 24 AA.
 AC Q8SH92;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia superciliaris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179895;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448778; AAL90614.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2562 MW; B22B1975311691CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 32

Q8SH89 PRELIMINARY; PRT; 24 AA.
 AC Q8SH89;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia therezieni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448779; AAL90617.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2560 MW; C95A197529B596BB CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 33

Q8SH87 PRELIMINARY; PRT; 24 AA.
 AC Q8SH87;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN NDI.
 OS Brookesia thieli.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
 OC NCBI_TaxID=179897;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
 Chamaeleonidae (Reptilia, Squamata).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448780; AAL90620.1; -
 KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2622 MW; BD171975311691CA CRC64;

Query Match 16.0%; Score 4; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
 ||||
 Db 21 AALP 24

RESULT 34

Q8SH84
ID Q8SH84 PRELIMINARY; PRT; 24 AA.
AC Q8SH84;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Brookesia tuberculata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Brookesia.
OX NCBI_TaxID=179898;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR MBL; AF448781; AAL90623.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 24 AA; 2560 MW; C95A197529B596BB CRC64;
Query Match 16.0%; Score 4; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 AALP 6
Db 21 AALP 24
RESULT 35
Q9AUE9 PRELIMINARY; PRT; 24 AA.
ID Q9AUE9;
AC Q9AUE9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Stearoyl-ACP desaturase (Fragment).
GN DELTA9-BN-1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DRAKKAR;
RA Fourmann M., Roger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
RT of Arabidopsis-known-function genes in Brassica.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF230689; AAK14946.1; -.
FT NON TER 1
FT NON TER 24
SQ SEQUENCE 24 AA; 2757 MW; 6C684EFD165113E0 CRC64;
Query Match 16.0%; Score 4; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 SLKK 22
Db 4 SLKK 7
RESULT 36
P82833 PRELIMINARY; PRT; 24 AA.
ID P82833;
AC P82833;
DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Brevinin-1BA.
OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=30360;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop P.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RL Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS.
CC -|- MASS SPECTROMETRY: MW=2643; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic.
FT DISULFID 18 24 BY SIMILARITY.
SQ SEQUENCE 24 AA; 2645 MW; CB524A454471DF4 CRC64;
Query Match 16.0%; Score 4; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GMAA 4
Db 7 GMAA 10
RESULT 37
P82834 PRELIMINARY; PRT; 24 AA.
ID P82834;
AC P82834;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE Brevinin-1BB.
OS Rana berlandieri (Rio Grande leopard frog) (Rana pipiens berlandieri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=30360;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=SKIN;
RX MEDLINE=20117700; PubMed=10651828;
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop P.C., Platz J.E.,
RA Conlon J.M.;
RT "Peptides with antimicrobial activity from four different families
RT isolated from the skins of the North American frogs Rana luteiventris,
RL Rana berlandieri and Rana pipiens.";
RL Eur. J. Biochem. 267:894-900(2000).
CC -|- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC S.AUREUS AND GRAM-NEGATIVE BACTERIUM E.COLI. ACTIVE AGAINST
CC C.ALBICANS.
CC -|- MASS SPECTROMETRY: MW=2567.3; METHOD=ELECTROSPRAY.
CC -|- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC FAMILY.
KW Antibiotic; Fungicide.
FT DISULFID 18 24 BY SIMILARITY.
SQ SEQUENCE 24 AA; 2569 MW; CB524A454147DF4 CRC64;
Query Match 16.0%; Score 4; DB 13; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GMAA 4
Db 7 GMAA 10

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Db 7 GMAA 10

RESULT 38
P82838 PRELIMINARY; PRT; 24 AA.
ID Q85452
AC Q85452;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain 349) gag-mos splice junction mRNA
DE (Fragment).
OC Moloney murine leukemia virus.
OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85108156; PubMed=3982040;
RA Nash M.A., Brizzard B.L., Wong J.L., Murphy E.C.Jr.;
RT "Murine sarcoma virus tel10 RNA transcripts: Origin from a single
RT proviral DNA and sequence of the gag-mos junctions in both the
RT precursor and spliced viral RNAs."
RL J. Virol. 53:624-633(1985).
DR EMBL; K02856; AAA46489.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2668 MW; 3D1AF681EBF3B1C6 CRC64;

Query Match 16.0%; Score 4; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 HFSL 20
DB 17 HFSL 20

RESULT 41
Q66113 PRELIMINARY; PRT; 7 AA.
ID Q66113
AC Q66113;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE C-terminus of the viral replicase (Fragment).
DE cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EEDC6D740 CRC64;

Query Match 12.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
DB 5 LPR 7

RESULT 42
O09258

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ID O09258 PRELIMINARY; PRT; 8 AA.
 AC O09258;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE NifH (Fragment)
 GN NifH
 OS Synecococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
 OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
 OX NCBI_TaxID=41431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RF-1;
 RX MEDLINE=9231861; PubMed=10217509;
 RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
 RT "Organization and expression of nitrogen-fixation genes in the aerobic
 RT nitrogen-fixing unicellular cyanobacterium Synecococcus sp. strain
 RT RF-1."
 RL Microbiology 145:743-753 (1999).
 DR MBL; AF001780; AAC33389.1; --
 FT NON TER 8
 SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;
 Query Match 12.0%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 IAF 11
 DB 4 IAF 6
 RESULT 43
 Q9AGP4 PRELIMINARY; PRT; 8 AA.
 ID Q9AGP4;
 AC Q9AGP4;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Serine hydroxymethyltransferase (Fragment).
 GN GLVA.
 OS Arthrobacter sp. 11N.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
 OX NCBI_TaxID=153502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=11N;
 RA Leskys R., Harris R.J., Casate V., Bastan J., Scrutton N.S.;
 RT "Genetic organization of the genes involved in dimethylglycine and
 RT sarcosine degradation in Arthrobacter spp.: implications for glycine
 RT betaine catabolism."
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF329478; AAK16486.1; --
 DR MBL; AF329478; AAK16486.1; --
 KW Methyltransferase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 898 MW; 6B1870533372457 CRC64;
 Query Match 12.0%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 LKK 22
 DB 3 LKK 5
 RESULT 44
 P82858 PRELIMINARY; PRT; 8 AA.
 ID P82858
 AC P82858;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Uricase (EC 1.7.3.3) (Urate oxidase) (Fragment).
 OS Puccinia recondita f. sp. triseti.
 OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
 OC Uredinales; Pucciniaceae; Puccinia.
 OX NCBI_TaxID=142679;
 RN [1]
 RP SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
 RC TISSUE=SPORE;
 RA Aguilar M., Montalbini P., Pineda M.;
 RL Submitted (NOV-2000) to the SWISS-PROT data bank.
 CC -|- FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
 CC AND FUNGI.
 CC -|- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
 CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
 CC -|- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
 CC -|- DEVELOPMENTAL STAGE: GERMINATION.
 CC -|- SIMILARITY: BELONGS TO THE URICASE FAMILY.
 DR INTERPRO: IPR002042; Uricase.
 DR PROSITE: PS00366; URICASE; PARTIAL.
 KW Oxidoreductase; Purine metabolism; Peroxisome.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 777 MW; 98C1ADD735B9D76D CRC64;
 Query Match 12.0%; Score 3; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 FSL 20
 DB 3 FSL 5
 RESULT 45
 Q9ERD2 PRELIMINARY; PRT; 8 AA.
 ID Q9ERD2;
 AC Q9ERD2;
 DT 01-WAR-2001 (TReMBLrel. 16, Created)
 DT 01-WAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-WAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Galactose-1-phosphate uridylyl transferase (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/D3;
 RA Leslie N.D., Bai S.;
 RT "Functional analysis of the mouse galactose-1-phosphate uridylyl
 RT transferase (GALT) promoter."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RW EMBL; AF314226; AAG31161.1; --
 KW Transferase.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 854 MW; ECBCD409DIADDD6 CRC64;
 Query Match 12.0%; Score 3; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MAA 4
 DB 1 MAA 3
 RESULT 46
 Q9QVK5 PRELIMINARY; PRT; 8 AA.
 ID Q9QVK5
 AC Q9QVK5
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

Thu Dec 19 17:47:46 2002

DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373341; PubMed=1832670;
 RA Hopper W., Beckert L., Buck F., Seitz H.J.;
 RT "Is the p29 protein involved in the rapid regulation of
 RT phosphoenolpyruvate carboxylase (GTP)?";
 RL J. Biol. Chem. 266:17257-17260(1991).
 SQ SEQUENCE 8 AA; 819 MW; C3672DCAEDD04AEA CRC64;

Query Match 12.0%; Score 3; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
 Db |||
 6 ALP 8

RESULT 47
 Q9R7H9 PRELIMINARY; PRT; 9 AA.
 ID Q9R7H9
 AC Q9R7H9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Lipoprotein (Fragment).
 GN NLPD.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98083063; PubMed=9422600;
 RA Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., Golomb M.;
 RT "The tryptophanase gene cluster of Haemophilus influenzae type b:
 RT evidence for horizontal gene transfer.";
 RL J. Bacteriol. 180:1107-1118(1998).
 DR EMBL; AF003252; AAB96582.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1152 MW; 35A017673B4412D7 CRC64;

Query Match 12.0%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
 Db |||
 6 LPR 8

RESULT 48
 Q14277 PRELIMINARY; PRT; 9 AA.
 ID Q14277
 AC Q14277
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE RT protein short form (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94071887; PubMed=7902707;
 RA Ceccherini I., Bocciaudi R., Luo Y., Pasini B., Hofstra R.,
 RA Takahashi M., Romeo G.;

"Exon structure and flanking intronic sequences of the human RET proto-oncogene.";
 RT Biochem. Biophys. Res. Commun. 196:1289-1295(1993).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94366753; PubMed=8084609;
 RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
 RA Bocciaudi R., Nijveen H., Bolino A., Sari M., Ronchetto P., Pasini B.,
 RA Bazzano M., Buys C., Romeo G.;
 RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
 RT the ret proto-oncogene";
 RL Oncogene 9:3025-3029(1994).
 DR EMBL; U11532; AAC50102.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 12.0%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
 Db |||
 5 APT 7

RESULT 49
 Q9TWVO PRELIMINARY; PRT; 9 AA.
 ID Q9TWVO
 AC Q9TWVO
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Antho-RPAMIDE=NEUROPEPTIDE.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthese; Actiniidae; Anthopleura.
 OC NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93126143; PubMed=1480510;
 RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
 RT "Isolation of Leu-Pro-Gly-Pro-Gly-Pro-Arg-Pro-NH2 (Antho-RPamide),
 RT an N-terminally protected, biologically active neuropeptide from sea
 RT anemones.";
 RL Peptides 13:851-857(1992).
 FT NON TER 1
 SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 12.0%; Score 3; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
 Db |||
 6 LPR 8

RESULT 50
 Q9TRW2 PRELIMINARY; PRT; 9 AA.
 ID Q9TRW2
 AC Q9TRW2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CALDESMON=PHOSPHORYLATION site (Fragment).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91378498; PubMed=1898046;
 RA Ikebe M., Hornick T.;
 RA "Determination of the phosphorylation sites of smooth muscle caldesmon

RA Jenkins N.A., Harbers K.;
RT "Structure of the gene encoding the ubiquitin-conjugating enzyme
RL UbcM4, characterization of its promoter, and chromosomal location.",
RL Gene 224:109-116(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Mueller U., Grams A., Martinez-Noel G., Harbers K.,
RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF071557; AAD10128.1; -
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; C90F97341415BDD CRC64;

Query Match 12.0%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 MAA 4
DB 1 MAA 3

RESULT 53
Q90350 PRELIMINARY; PRT; 9 AA.
ID Q90350
AC Q90350; (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OC NCBI_TaxID=45255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SG3419;
RX MEDLINE=99266893; PubMed=10335862;
RA Wong S.B.J., Chan S.H., Ren E.C.,
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
RT predominance of group 2a and the Asian group 3 variant.",
RL J. Med. Virol. 58:145-153(1999).
DR EMBL; AF078065; AAC32371.1; -
FT NON TER 9
SQ SEQUENCE 9 AA; 989 MW; D95CA5A5BEB9CDDD CRC64;

Query Match 12.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 MAA 4
DB 1 MAA 3

RESULT 54
Q9E1U7 PRELIMINARY; PRT; 9 AA.
ID Q9E1U7
AC Q9E1U7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE X protein (Fragment).
GN X.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2F-8;
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in

by protein kinase C.";
Arch. Biochem. Biophys. 288:538-542(1991).
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;

Query Match 12.0%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 19 SLK 21
DB 3 SLK 5

RESULT 51
Q988J8 PRELIMINARY; PRT; 9 AA.
ID Q988J8
AC Q988J8;
DT 1-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ORYZATENSIN-BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.",
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 12.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 5 LPR 7
DB 7 LPR 9

RESULT 52
Q88889 PRELIMINARY; PRT; 9 AA.
ID Q88889
AC Q88889; (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ubiquitin-conjugating enzyme UBCM4 (Fragment).
GN UBCM4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97057256; PubMed=8901595;
RA Harbers K., Muller U., Grams A., Li E., Jaenisch R., Franz T.;
RT "Provirus integration into a gene encoding a ubiquitin-conjugating
RT enzyme results in a placental defect and embryonic lethality.",
RL Proc. Natl. Acad. Sci. U.S.A. 93:12412-12417(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99132641;
RA Mller U., Grams A., Martinez-Noel G., Copeland N.G., Gilbert D.J.,


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RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276526; AAG29993.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 994 MW; CD0FDEBEA2D40DDD CRC64;

Query Match 12.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
Db 1 MAA 3

RESULT 55
Q9X533 PRELIMINARY; PRT; 10 AA.
ID Q9X533
AC Q9X533;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RL bacteria isolated from the fecal flora of primates.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=209A;
RX MEDLINE=20568355; PubMed=11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT "The quality of merC, a module of the mer mosaic.";
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL; AF120964; AAD23783.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A7B58 CRC64;

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
Db 7 SLK 9

Search completed: December 19, 2002, 17:43:41
Job time : 29 secs

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Thu Dec 19 17:47:38 2002

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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 / Search time 34 Seconds
(without alignments)
97.978 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GMAALPRLIAFTSEHSLSLKGA 25

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 320054

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

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4: /SID22/cgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/cgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/cgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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8: /SID22/cgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/cgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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23: /SID22/cgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	25	100.0	25 16 AAR8667	Human glutamic aci
2	25	100.0	25 18 AAW18848	65 KD Glutamic aci
3	16	64.0	20 16 AAR72279	Glutamic acid deca
4	16	64.0	20 21 AAY59552	GAD65 fragment, pe
5	14	56.0	20 16 AAR72278	Glutamic acid deca
6	14	56.0	20 21 AAY59578	GAD65 fragment, pe
7	9	36.0	20 21 AAY57065	Glutamate decarbox
8	8	32.0	24 21 AAB07785	Glutamic acid deca
9	6	24.0	19 18 AAW36759	Thrombopoietin rec
10	6	24.0	19 18 AAW09608	Thrombopoietin rec

11	6	24.0	19	22	AAU25978	Human thrombopoiet
12	5	20.0	8	16	AAW21217	Farnesyl synthetas
13	5	20.0	8	22	AAJ00161	Hepatitis C virus
14	5	20.0	8	22	AAJ00801	Hepatitis C virus
15	5	20.0	8	22	AAJ01077	Hepatitis C virus
16	5	20.0	8	22	AAJ01728	Hepatitis C virus
17	5	20.0	8	22	AAJ02447	Hepatitis C virus
18	5	20.0	8	22	AAJ02598	Hepatitis C virus
19	5	20.0	8	22	AAJ02836	Hepatitis C virus
20	5	20.0	8	22	AAJ02983	Hepatitis C virus
21	5	20.0	9	18	AAW43336	Immunogenic HLA-A2
22	5	20.0	9	21	AAJ73109	Hepatitis C virus
23	5	20.0	9	22	AAJ00023	Hepatitis C virus
24	5	20.0	9	22	AAJ00689	Hepatitis C virus
25	5	20.0	9	22	AAJ01005	Hepatitis C virus
26	5	20.0	9	22	AAJ01837	Hepatitis C virus
27	5	20.0	9	22	AAJ02599	Hepatitis C virus
28	5	20.0	9	22	AAJ02963	Hepatitis C virus
29	5	20.0	9	22	AAJ03126	Hepatitis C virus
30	5	20.0	9	22	AAJ03222	Hepatitis C virus
31	5	20.0	9	22	AAJ03432	Hepatitis C virus
32	5	20.0	9	22	AAJ03529	Hepatitis C virus
33	5	20.0	9	22	AAJ03614	Hepatitis C virus
34	5	20.0	9	22	AAJ03788	Hepatitis C virus
35	5	20.0	9	22	AAJ03867	Hepatitis C virus
36	5	20.0	9	22	AAJ03956	Hepatitis C virus
37	5	20.0	9	22	AAJ03965	Hepatitis C virus
38	5	20.0	9	22	AAJ04087	Hepatitis C virus
39	5	20.0	9	22	AAJ76345	Human secreted pro
40	5	20.0	9	22	AAJ59489	Immunogenic peptid
41	5	20.0	9	23	AAU95868	Peptide derived fr
42	5	20.0	10	17	AAW01985	Human complementar
43	5	20.0	10	22	AAJ96799	Hepatitis C virus
44	5	20.0	10	22	AAJ01931	Hepatitis C virus
45	5	20.0	10	22	AAJ02783	Hepatitis C virus
46	5	20.0	11	16	AAW21218	Farnesyl synthetas
47	5	20.0	11	22	AAJ00088	Hepatitis C virus
48	5	20.0	11	22	AAJ00671	Hepatitis C virus
49	5	20.0	11	22	AAJ00826	Hepatitis C virus
50	5	20.0	11	22	AAJ00842	Hepatitis C virus
51	5	20.0	11	22	AAJ01943	Hepatitis C virus
52	5	20.0	11	22	AAJ02021	Hepatitis C virus
53	5	20.0	11	22	AAJ02097	Hepatitis C virus
54	5	20.0	11	22	AAJ02448	Hepatitis C virus
55	5	20.0	11	22	AAJ02600	Hepatitis C virus
56	5	20.0	11	22	AAJ02837	Hepatitis C virus
57	5	20.0	11	22	AAJ02922	Hepatitis C virus
58	5	20.0	12	15	AAJ67053	Neurotrophic Facto
59	5	20.0	14	16	AAJ67638	Epitope of Non-A
60	5	20.0	14	22	AAJ00613	Human protein frag
61	5	20.0	14	22	AAJ00614	Human protein frag
62	5	20.0	15	19	AAW85435	Helper T-cell clas
63	5	20.0	15	19	AAW85271	Helper T-cell pept
64	5	20.0	15	19	AAW85282	Helper T-cell pept
65	5	20.0	15	21	AAJ73095	Hepatitis C virus
66	5	20.0	15	22	ABG27780	Novel human diagno
67	5	20.0	15	22	AAJ03084	Hepatitis C virus
68	5	20.0	15	22	AAJ03180	Hepatitis C virus
69	5	20.0	15	22	AAJ03267	Hepatitis C virus
70	5	20.0	15	22	AAJ03390	Hepatitis C virus
71	5	20.0	15	22	AAJ03487	Hepatitis C virus
72	5	20.0	15	22	AAJ03572	Hepatitis C virus
73	5	20.0	15	22	AAJ03657	Hepatitis C virus
74	5	20.0	15	22	AAJ04013	Hepatitis C virus
75	5	20.0	15	22	AAJ04014	Hepatitis C virus

ALIGNMENTS

RESULT 1
AAR8667
ID AAR8667 standard; peptide; 25 AA.

XX AAR88667;
AC
XX 05-MAR-1996 (first entry)
DT
XX Human glutamic acid decarboxylase residues 266-290.
DE
XX diabetes; T-cell subpopulation; detection; antigen production;
KW diagnosis; autoimmune disease.
XX Homo sapiens.
XX DE4418091-A1.
PN
XX 27-JUL-1995.
PD
XX 24-MAY-1994; 94DE-4418091.
PF
XX 04-FEB-1994; 94DE-4403522.
PR
XX 0-JAN-1994; 94DE-4401629.
PF
XX (ENDL/) ENDL J.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PA
XX Albert W, Dornmair K, Endl J, Jung G, Meinel E;
PI Stahl P, Schendel D;
PI
XX WPI; 1995-264505/35.
DR
XX Antigen-specific activated T-lymphocytes and their detection - by
XX interaction with inventive peptide(s) of peptide-MHC complexes;
XX useful in diagnosis of e.g. diabetes and autoimmune diseases
XX
XX Claim 1; Page 13; 21pp; German.
XX
XX AAR88667 is derived from residues 266-290 of human glutamic acid
XX decarboxylase and specifically reacts with a T-cell sub-population
XX isolated from recently diagnosed Type-I diabetics. Pharmaceutical
XX compns. contg. this peptide and those shown in AAR88668 and
XX AAR76642-62, are useful for the diagnosis of a disease or predispositions
XX of immune system diseases, tumours, and autoimmune diseases, including
XX diabetes. The peptides are able to detect specific T-cell subpopulations
XX that are then used for antigen prodn., e.g. by reinjection.
XX
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 25; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e-18; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;
QY 1 GMAALPRLIAPTSEHSFSLKKGAA 25
DB 1 GMAALPRLIAPTSEHSFSLKKGAA 25
RESULT 2
AAR18848
ID AAR18848 standard; peptide; 25 AA.
AC
XX AAR18848;
XX
XX 05-JAN-1998 (first entry)
DT
XX 65 kD Glutamic acid decarboxylase peptide fragment VII.
DE
XX GAD, 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
XX insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KW predisposition; autoimmune; tumour; rheumatoid arthritis;
KW multiple sclerosis.
XX Synthetic.
XX
XX DE19526561-A1.
PN

XX 23-JAN-1997.
PD
XX 20-JUL-1995; 95DE-1026561.
PF
XX 20-JUL-1995; 95DE-1026561.
PR
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
PA
XX Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;
PI Porzilli P, Stahl P;
PI
XX WPI; 1997-088254/09.
DR
XX Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
XX involving intradermal admin. of auto:reactive substances
XX
XX Claim 11; Page 10; 12pp; German.
XX
XX AAW18842-70 are peptide fragments of the 65 kD human glutamic acid
XX decarboxylase (GAD). The fragments are autoreactive substances used for
XX diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis
XX is determined by using a claimed method for diagnosis of cell-mediated
XX diseases or a predisposition to cell-mediated diseases, which is
XX effected by administering an autoreactive substance intradermally and
XX establishing the diagnosis on the basis of the occurrence or lack of a
XX positive reaction at the site of administration. The method is used for
XX diagnosis of autoimmune and tumour diseases, preferably T-cell-mediated
XX diseases such as rheumatoid arthritis, multiple sclerosis and especially
XX IDDM.
XX
XX Sequence 25 AA;
SQ
Query Match 100.0%; Score 25; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e-18; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;
QY 1 GMAALPRLIAPTSEHSFSLKKGAA 25
DB 1 GMAALPRLIAPTSEHSFSLKKGAA 25
RESULT 3
AAR72279
ID AAR72279 standard; Peptide; 20 AA.
AC
XX AAR72279;
XX
XX 13-NOV-1995 (first entry)
DT
XX Glutamic acid decarboxylase (GAD65) fragment.
DE
XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
KW insulin-dependant diabetes mellitus; stiff man disease.
XX
XX Homo sapiens.
XX
XX WO9507992-A.
PN
XX 23-MAR-1995.
PD
XX 24-AUG-1994; 94WO-US09478.
PF
XX 17-SEP-1993; 93US-0123859.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Clare-Salzler MJ, Brandler MG, Kaufman DL, Tobin AJ;
PI WPI; 1995-131360/17.
PI
XX New polypeptide fragments of glutamic acid decarboxylase - for
XX diagnosis and treatment of autoimmune disease, esp. insulin
XX

PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.
XX Example 11; Page 76; 100pp; English.
XX AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human
CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in AAR72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
XX SQ Sequence 20 AA;
Query Match 64.0%; Score 16; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 APTSEHSHFSLKKGAA 25
Db 1 APTSEHSHFSLKKGAA 16
RESULT 4
AAY59552
ID AAY59552 standard; peptide; 20 AA.
XX AC AAY59552;
XX DT 03-APR-2000 (first entry)
XX DE GAD65 fragment, peptide #19.
XX KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
XX KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
XX KW therapy.
XX OS Homo sapiens.
XX PN US5998366-A.
XX PD 07-DEC-1999.
XX PF 09-APR-1997; 97US-0827618.
XX PR 07-JUN-1995; 95US-0485725.
XX PR 21-SEP-1990; 90US-0586536.
XX PR 18-JUN-1991; 91US-0718909.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Tobin AJ, Kaufman DL, Erlander MG;
XX DR WPI; 2000-095930/08.
XX PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and Stiff man
PT disease -
XX Claim 1; Column 42; 61pp; English.
XX This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX

SQ Sequence 20 AA;
Query Match 64.0%; Score 16; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 APTSEHSHFSLKKGAA 25
Db 1 APTSEHSHFSLKKGAA 16
RESULT 5
AAR72278
ID AAR72278 standard; Peptide; 20 AA.
XX AC AAR72278;
XX DT 13-NOV-1995 (first entry)
XX DE Glutamic acid decarboxylase (GAD65) fragment.
XX KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
XX KW insulin-dependant diabetes mellitus; stiff man disease.
XX OS Homo sapiens.
XX PN WO9507992-A.
XX PD 23-MAR-1995.
XX PF 24-AUG-1994; 94WO-US09478.
XX PR 17-SEP-1993; 93US-0123859.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
XX DR WPI; 1995-131360/17.
XX PT New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease, esp. insulin
PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.
XX Example 11; Page 76; 100pp; English.
XX AAQ86481 and AAQ86482 encode AAR71733 and AAR79105, rat and human
CC glutamic acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in AAR72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
XX SQ Sequence 20 AA;
Query Match 56.0%; Score 14; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GMAALPRLIAPTSE 14
Db 7 GMAALPRLIAPTSE 20
RESULT 6
AAY59578
ID AAY59578 standard; peptide; 20 AA.
XX AC AAY59578;
XX DT 03-APR-2000 (first entry)
XX

DE GAD65 fragment, peptide #18.
 XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 OS
 XX US998366-A.
 PN
 XX 07-DEC-1999.
 PD
 XX 09-APR-1997; 97US-0827618.
 PF
 XX 07-JUN-1995; 95US-0485725.
 PR
 XX 21-SEP-1990; 90US-0586536.
 PR
 XX 18-JUN-1991; 91US-0716909.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Robin AJ, Kaufman DL, Erlander MG;
 PI WPI; 2000-095930/08.
 XX
 DR Ameliorating glutamic acid decarboxylase associated autoimmune
 XX disorders such as insulin dependent diabetes mellitus and Stiff man
 PT disease -
 PT
 XX Example 11; Column 42; 61pp; English.
 PS
 XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 CC
 XX Sequence 20 AA;
 SQ
 Query Match 56.0%; Score 14; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMAALPRLIAFTSE 14
 DB 7 GMAALPRLIAFTSE 20
 RESULT 7
 AAY57065
 ID AAY57065 standard; peptide; 20 AA.
 XX
 AC AAY57065;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Glutamate decarboxylase peptide GAD p18.
 XX
 KW Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX
 XX Homo sapiens.
 OS
 XX WO9956763-A1.
 PN
 XX 11-NOV-1999.
 PD

XX 07-MAY-1999; 99WO-US10250.
 XX
 XX 07-MAY-1998; 98US-0084636.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Kaufman DL, Tian J, Olcott A;
 PI WPI; 2000-052905/04.
 DR
 XX Administration of neglected target tissue antigens to modulate immune
 PT responses -
 PT
 XX Disclosure; Page 23; 79pp; English.
 PS
 XX Amino acid sequences AAY57063-Y57091 are examples of neglected target
 CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
 CC not involved in autoimmunity. These peptides and proteins are used in
 CC the method of the invention which involves administering an NNTA as an
 CC antigen based immunotherapeutic agent, to a host afflicted with an
 CC autoimmune response associated with an autoimmune disease. The
 CC immunotherapeutic agent is used to treat autoimmune diseases such as
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
 CC inflammatory immune responses. The NNTA induces regulatory tolerance by
 CC elicitation of regulatory T cells among T cells recognizing the NNTA but
 CC not participating in the immune response. The NNTA are capable of
 CC recognition by substantial populations of uncommitted T cells which can
 CC be primed, or biased, towards regulatory responses to provide effective
 CC treatment. The NNTA are effective in regulating undesirable immune
 CC responses even when target determinants used as agents promoting
 CC tolerance agents have failed to induce an effective regulatory T cell
 CC response. NNTAs as agents promoting tolerance are anticipated to be safer
 CC than use of target determinants.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 36.0%; Score 9; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 PRLIAFTSE 14
 DB 12 PRLIAFTSE 20
 RESULT 8
 AAB07785
 ID AAB07785 standard; peptide; 24 AA.
 XX
 AC AAB07785;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Glutamic acid decarboxylase-65 (GAD-65) analogue peptide.
 XX
 KW Glutamic acid decarboxylase-65; GAD-65; autoimmune disease;
 KW insulin-dependent diabetes mellitus; IDDM; stiff man syndrome;
 KW cellular autoimmune response; T-cell receptor; autoimmune antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Key
 FT Misc-difference 15
 FT /label= Thr, Glu
 XX
 XX EP1026238-A2.
 PN
 XX 09-AUG-2000.
 PD
 XX 17-JUN-1992; 2000EP-0102229.
 PP
 XX

CC The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from CC chemotherapy, radiation therapy or bone marrow transfusions. The CC peptide may also be used to maintain the proliferation and growth of CC TPO-dependent cell lines and for use in biological research, for CC detecting TPO receptors on living cells.

XX

XX Sequence 19 AA;

Query Match 24.0%; Score 6; DB 18; Length 19;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25

DB 10 LKKGAA 15

RF 11

AA 78

ID AAU25978 standard; Peptide; 19 AA.

XX

AC AAU25978;

XX

DT 17-DEC-2001 (first entry)

XX

DE Human thrombopoietin receptor (TPO-R) activator peptide #164.

XX

KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; KW bone marrow transplantation; haematological disorder; platelet disorder; KW enzyme-linked immunosorbent assay; in situ staining; biological fluid; KW tissue homogenate; fluorescence-activated cell sorting; Western blotting; KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX

OS Homo sapiens.

XX

XX US6251864-B1.

PN

XX

XX 26-JUN-2001.

PD

XX

XX 01-MAR-2000; 2000US-0516704.

PP

XX

XX 07-JUN-1995; 95US-0478128.

PR

XX

XX 07-JUN-1995; 95US-0485301.

PR

XX

XX 07-JUN-1996; 96WO-US09623.

PR

XX

XX 5-AUG-1996; 96US-0699027.

PR

XX

PA (GLAXO) GLAXO GROUP LTD.

XX

XX

PI Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz RJ;

PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB;

PI Podduturi S, Yin Q;

XX

XX WPI; 2001-564142/63.

DR

XX

XX Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and haematological disorders, comprises contacting

PT cells with peptides and peptide mimetics attached to hydrophilic

PT polymers -

XX

XX Disclosure; Column 23; 128pp; English.

XX

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods CC of activating thrombopoietin receptors in cells comprise contacting the CC cells with effective amounts of peptides and peptide mimetics attached to CC hydrophilic polymers. The methods are used to treat thrombocytopenia such CC as that due to chemotherapy, radiation therapy or bone-marrow CC transplantation and to prevent thrombocytopenia in patients at risk. The CC sequences are used to treat and prevent haematological disorders CC including thrombocytopenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living CC cells and fixed cells, in biological fluids, in tissue homogenates, and CC in purified or natural biological materials. They may also be used for in CC situ staining, fluorescence-activated cell sorting, Western blotting and CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can CC be used for in vitro expansion of megakaryocytes and their committed CC progenitors alone or in conjunction with additional cytokines.

XX

XX Sequence 19 AA;

Query Match 24.0%; Score 6; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25

DB 10 LKKGAA 15

RESULT 12

AAW21217

ID AAW21217 standard; peptide; 8 AA.

XX

AC AAW21217;

XX

DT 29-JUL-1997 (first entry)

XX

DE Farnesyl synthetase derived signal oligopeptide #17.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV; KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor; KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1; KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus; KW gonadolibin precursor; plasminogen activator inhibitor 2; prorenin; KW Alzheimer amyloid A4; corticotropin releasing factor binding protein; KW apolipoprotein B; herpes virus 1 glycoprotein B; HSV1; human; OMVVS; KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A; KW Treponema pallidum membrana protein; TMPA; islet amyloid polypeptide; KW fibroblast MMP1; schistosoma elastase precursor; schistosomin; KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

XX WO9519568-A1.

PN

XX

XX 20-JUL-1995.

PD

XX

XX 12-JAN-1995; 95WO-US00575.

PP

XX

XX 14-JAN-1994; 94US-0182248.

PR

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

XX WPI; 1995-263953/34.

DR

XX

XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as

PT regions of max. hydrophilicity, used in modulating communication

PT between protein(s)

XX

XX Claim 5; Page 25; 88pp; English.

XX

XX The sequences given in AAW21201-560 represent hydrophilic signal oligo- CC peptides. These signal oligopeptides are localised on the surface CC of the protein and are represented by the hydrophilicity maxima of CC the protein. These peptides are enriched in charged amino acids CC arranged with neutral spacer amino acids. The specific signal CC character of these oligopeptides is determined by a characteristic CC combination of conformation and charge within the signal sequence. CC These oligopeptides may be used as vaccines in the treatment of

CC human disease, as competitive inhibitors to prevent or reduce the
 CC metabolic action or interaction of a selected protein by blocking
 CC its specific signal sequences, or as therapeutic agents to function
 CC as feedback regulators to reduce synthesis rate of a selected protein.
 CC These peptides may be modified by omitting one or more amino acids at
 CC the N- and/or C-terminal, by substituting one or more amino acids
 CC without consideration of charge and polarity, by substituting one or
 CC more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSLKK 22
 DB 2 FSLKK 6
 |||||

RESULT 13

AAJ00161
 ID AAJ00161 standard; Peptide; 8 AA.

XX AC AAJ00161;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #152.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PL Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus -
 XX PS Disclosure; Page 104; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 4 RLIAF 8
 |||||

RESULT 14

AAJ00801
 ID AAJ00801 standard; Peptide; 8 AA.

XX AC AAJ00801;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #792.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PL Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus -
 XX PS Disclosure; Page 120; 214pp; English.

XX CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 8 AA;

Query Match 20.0%; Score 5; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 1 RLIAF 5
 |||||

RESULT 15

AAJ01077
 ID AAJ01077 standard; Peptide; 8 AA.

XX AC AAJ01077;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #1069.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX XX

PA (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 127; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 8;
 XX Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8

RESULT 16
 AAJ01728
 ID AAJ01728 standard; Peptide; 8 AA.
 XX AAJ01728;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #1719.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 160; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Query Match 20.0%; Score 5; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 1 RLIAF 5

RESULT 17
 AAJ02447
 ID AAJ02447 standard; Peptide; 8 AA.
 XX AAJ02447;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #2438.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.
 XX 29-MAR-2001.
 XX 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 160; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 8 AA;
 XX Query Match 20.0%; Score 5; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 1 RLIAF 5

RESULT 18
 AAJ02598
 ID AAJ02598 standard; Peptide; 8 AA.
 XX AAJ02598;
 XX 02-JUL-2001 (first entry)
 DE Hepatitis C virus epitope #2589.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 XX WO200121189-A1.

[illegible]

XX Immunogen; binding motif; HLA-A2.1 allele; immunogenic peptide; cancer;
 KW glycoprotein; T cell activation; immune response; hepatitis C virus;
 KW human immunodeficiency virus type 1; HIV-1; vaccine; infection; antigen;
 KW HCV; HBV.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN WO9734621-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 21-MAR-1997; 97WO-US05348.
 XX
 PR 20-MAR-1997; 97US-0822382.
 PR 21-MAR-1996; 96US-0013980.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Grey HM, Sette A, Sidney J;
 XX
 DR WPI, 1997-479987/44.
 XX
 PT HLA-A2.1 binding peptide(s) - used in vaccines for the treatment and
 PT prevention of e.g. viral infection and cancer
 XX
 PS Claim 4; Page 29; 39pp; English.
 XX
 CC This sequence is an example of an immunogenic peptide having an HLA-A2.1
 CC binding motif, which is capable of inducing a T cell activation in T
 CC cells restricted by the A2.1 allele. This peptide is useful in eliciting
 CC an immune response against hepatitis C virus (HCV). The invention relates
 CC to a group of peptides having an HLA-A2.1 binding motif comprising 9 or
 CC 10 residues in which there is a first conserved residue at position 2
 CC selected from Leu, Met, Ile, Val, Ala and Thr and a second conserved
 CC residue at the C-terminus (position 9 or 10) selected from Val, Leu,
 CC Ile, Ala and Met. The immunogens are viral, e.g. human immunodeficiency
 CC virus type I (HIV-1), hepatitis B virus (HBV) and hepatitis C virus (HCV)
 CC or cancer antigens and are used in vaccines for the prevention and
 CC treatment of viral infection and cancer. The immunogens may be
 CC administered to the patient as a nucleic acid encoding the peptide
 CC (gene vaccine).
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 18; Length 9;
 Local Similarity 100.0%; Pred. No. 7.8e+05;
 Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8
 RESULT 22
 AAAY73109
 ID AAAY73109 standard; Peptide; 9 AA.
 XX
 AC AAAY73109;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Hepatitis C virus (HCV)-derived MHC class I (CTL) epitope, #267.
 XX
 KW Chimeric; pan DR epitope; expression vector;
 KW promoter; major histocompatibility complex; MHC; targeting; peptide;
 KW epitope; antigen; presentation; class I; cytosolic pathway;
 KW endoplasmic reticulum; class II; extracellular antigen;
 KW endocytic pathway; helper T lymphocyte; HTL; universal epitope;
 KW cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
 KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
 KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;

KW autoimmune disease; activation; antiviral; antimalarial;
 KW immunoprotective.
 XX
 OS Synthetic.
 OS Hepatitis C virus.
 XX
 PN WO9958658-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-US10646.
 XX
 PR 13-MAY-1998; 98US-0078904.
 PR 15-MAY-1998; 98US-0085751.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 PI Chesnut RW;
 XX
 DR WPI; 2000-039103/03.
 XX
 PT Expression vectors encoding major histocompatibility targeting
 PT sequence, used as, e.g. tumor vaccines -
 XX
 PS Claim 11; Page 68; 130pp; English.
 XX
 CC Sequences AAAY73103-Y73145 represent hepatitis C virus (HCV)-derived MHC
 CC class I (CTL) epitopes which are claimed for use in the present
 CC invention. The invention relates to a novel expression vector comprising
 CC a promoter operably linked to a fusion gene encoding a major
 CC histocompatibility complex (MHC) targeting sequence, and two or more
 CC heterologous peptide epitopes. The MHC targeting sequence may be a
 CC class I targeting sequence, which directs an MHC class I epitope to
 CC a cytosolic pathway or to the endoplasmic reticulum, or an MHC class
 CC II targeting sequence, which directs extracellular antigens to
 CC enter the endocytic pathway to be processed into antigen peptides
 CC for presentation on MHC class II molecules. The heterologous
 CC epitopes may comprise either helper T lymphocyte (HTL) epitopes,
 CC or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
 CC epitope such as a pan DR epitope (PADRE). The vectors are useful
 CC for stimulating an immune response in vivo, as well as for use in
 CC assaying the human immunogenicity of a human T cell peptide epitope in
 CC vivo in a non-human mammal. They provide a nucleic acid vaccine for
 CC enhancing immunity against infectious pathogens, such as viruses (e.g.,
 CC HIV, hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,
 CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
 CC autoimmune diseases. Universal MHC class II epitopes are advantageously
 CC combined with other MHC class I and class II epitopes to increase the
 CC number of cells that are activated in response to a given antigen and
 CC provide a broader population coverage of MHC-reactive alleles.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 Db 4 RLIAF 8
 RESULT 23
 AAAY00023
 ID AAAY00023 standard; Peptide; 9 AA.
 XX
 AC AAAY00023;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #14.

XX AAJ01837;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #1828.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX
 OS Hepatitis C virus.
 XX
 FN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Disclosure; Page 146; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 RLIAF 11
 DB 4 RLIAF 8
 RE . 27
 AAJ02599
 ID AAJ02599 standard; Peptide; 9 AA.
 XX
 AC AAJ02599;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #2590.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX
 OS Hepatitis C virus.
 XX
 FN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Disclosure; Page 146; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 RLIAF 11
 DB 4 RLIAF 8
 RE . 27
 AAJ02599
 ID AAJ02599 standard; Peptide; 9 AA.
 XX
 AC AAJ02599;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #2590.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX
 OS Hepatitis C virus.
 XX
 FN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Disclosure; Page 164; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 28
 AAJ02963
 ID AAJ02963 standard; Peptide; 9 AA.
 XX
 AC AAJ02963;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #2954.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX
 OS Hepatitis C virus.
 XX
 FN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Disclosure; Page 172; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 RLIAF 11

Db 5 RLIAF 9

RESULT 29

AAJ03126
ID AAJ03126 standard; Peptide; 9 AA.

XX AC AAJ03126;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3117.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

OS Hepatitis C virus.

XX PN WO200121189-A1.

XX XX 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 175; 21app; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RLIAF 11

Db 3 RLIAF 7

RESULT 30

AAJ03222
ID AAJ03222 standard; Peptide; 9 AA.

XX AC AAJ03222;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3213.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

OS Hepatitis C virus.

XX PN WO200121189-A1.

XX XX 29-MAR-2001.

XX 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 176; 21app; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

XX SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RLIAF 11

Db 4 RLIAF 8

RESULT 31

AAJ03432
ID AAJ03432 standard; Peptide; 9 AA.

XX AC AAJ03432;

DT 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #3423.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX KW antiviral.

OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX PT A new composition useful as a vaccine against hepatitis C virus

XX PS Disclosure; Page 178; 21app; English.

XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.

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Thu Dec 19 17:47:38 2002

SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 3 RLIAF 7
 RESULT 32
 AAJ03529
 ID AAJ03529 standard; Peptide; 9 AA.
 XX
 AC AAJ03529;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE hepatitis C virus epitope #3520.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 PS Disclosure; Page 180; 214pp; English.
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 20.0%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 34
 AAJ03788
 ID AAJ03788 standard; Peptide; 9 AA.
 XX
 AC AAJ03788;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #3779.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 PS Disclosure; Page 187; 214pp; English.

XX The present invention describes a composition comprising a prepared
CC Hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
SQ Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
| | | | |
DB 4 RLIAF 8

RESULT 35
AAJ03867
ID AAJ03867 standard; Peptide; 9 AA.
XX
AC AAJ03867;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3858.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
XX WO200121189-A1.
XX
PN 19-JUL-2000; 2000WO-US19774.
XX
PD 19-JUL-1999; 99US-0357737.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 2; Page 191; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
| | | | |
DB 4 RLIAF 8

RESULT 36
AAJ03956
ID AAJ03956 standard; Peptide; 9 AA.
XX

AC AAJ03956;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3947.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
OS Hepatitis C virus.
XX
XX WO200121189-A1.
XX
PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
PF 19-JUL-1999; 99US-0357737.
XX
PR
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 2; Page 195; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
| | | | |
DB 5 RLIAF 9

RESULT 37
AAJ03965
ID AAJ03965 standard; Peptide; 9 AA.
XX
AC AAJ03965;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #3956.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
OS Hepatitis C virus.
XX
XX WO200121189-A1.
XX
PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
PF 19-JUL-1999; 99US-0357737.
XX
PR
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Cellis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 2; Page 195; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
| | | | |
DB 5 RLIAF 9

PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-308046/32.
XX A new composition useful as a vaccines against hepatitis C virus -
XX
XX Example 3; Page 196; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
|||||
DB 4 RLIAF 8
RESULT 38
AAJ04087
ID AAJ04087 standard; Peptide; 9 AA.
XX
XX AAJ04087;
AC
XX
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #4078.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
KW
XX
XX Hepatitis C virus.
OS
XX
XX WO200121189-A1.
FN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX .EPIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
FI
XX
XX WPI; 2001-308046/32.
DR
XX
XX A new composition useful as a vaccines against hepatitis C virus -
FI
XX
XX Example 7; Page 203; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
|||||
DB 4 RLIAF 8

Db 4 RLIAF 8

RESULT 39
AAB76345
ID AAB76345 standard; Peptide; 9 AA.
XX
XX AAB76345;
AC
XX
XX 10-APR-2001 (first entry)
DT
XX
XX Hepatitis C virus immunogenic peptide..
DE
XX
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
KW HLA binding peptide; immune response; glycoprotein; cytostatic;
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
KW human immunodeficiency virus; proteoacide; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
KW condyloma acuminatum.
KW
XX
XX Hepatitis C virus.
OS
XX
XX WO200100225-A1.
FN
XX
XX 04-JAN-2001.
PD
XX
XX 28-JUN-2000; 2000WO-US17842.
PF
XX
XX 29-JUN-1999; 99US-0141422.
PR
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S;
PI WPI; 2001-112389/12.
FI
XX
XX Composition comprising human leukocyte antigen binding peptide which
PT comprises isolated, prepared epitope useful for treating viral
PT infections such as acquired immunodeficiency syndrome, and cancer -
XX
XX
XX Claim 1; Page 54; 58pp; English.
PS
XX
XX The present invention describes a composition (I) which comprises at
CC least one human leukocyte antigen (HLA) binding peptide comprising an
CC isolated, prepared epitope comprising one of 347 8-11 residue amino acid
CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
CC immunodeficiency virus) and proteoacide activities, which can be used
CC in vaccine production and is an inducer of cytotoxic T-cell response.
CC (I) is useful for inducing a cytotoxic T cell response against a
CC preslected antigen in a patient expressing a specific major
CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
CC treat and/or prevent viral infection and cancer such as prostate cancer,
CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
CC acuminatum.
XX
XX Sequence 9 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
|||||
DB 5 RLIAF 9

RESULT 40
AAB59489
ID AAB59489 standard; Peptide; 9 AA.

AC AAB59489,
XX
XX
XX 22-MAR-2001 (first entry)
XX
XX
XX Human secreted protein #25.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.

XX Homo sapiens.
XX
XX WO2000077173-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US14929.

XX 11-JUN-1999; 99US-0138573.

XX 07-JAN-2000; 2000US-0174851.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-071268/08.

XX N-PSDE; AAF23918.

XX Nucleic acids encoding 42 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating immune, hyperproliferative,
XX cardiovascular and neurological disorders or infectious diseases -

XX Claim 11; Page 430; 440pp; English.

XX Sequences AAB59465-B59506 represent the amino acid sequences of 42
XX human secreted proteins encoded by the genes AAF23894-P23935. The genes
XX and proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated from
XX a range of human tissues disclosed in the specification. The nucleic
XX acids, proteins, antibodies and (ant)agonists are useful in the
XX diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer, and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections.

XX Sequence 9 AA;

Query Match 20.0%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSE 14
DB 5 AFTSE 9

RESULT 41

AAU95868

ID AAU95868 standard; Peptide; 9 AA.

XX
XX AAU95868;

XX

02-JUL-2002 (first entry)

Immunogenic peptide with (HLA)-A2.1 binding site #81.

XX HLA-A2.1 binding peptide; cytostatic; virucide; anti-HIV; hepatotropic;
XX human immunodeficiency virus; antiinflammatory; antibacterial; vaccine;
XX protozoacide; immunosuppressant; immunogenic peptide; T cell activation;
XX human leucocyte antigen binding site; cytotoxic T cell response;
XX viral infection; hepatitis; Epstein-Barr virus; papilloma virus;
XX human immunodeficiency virus; HIV; Kaposi sarcoma; lymphoma;
XX cytomegalovirus; tumour; prostate cancer; renal carcinoma; lymphoma;
XX prostate-specific antigen; p53; carcino-embryonal antigen;
XX melanoma antigen; Mycobacterium tuberculosis; protozoa;
XX trypanosome surface antigen; condyloma acuminatum.

OS Hepatitis C virus.

XX WO200220616-A1.

XX 14-MAR-2002.

XX 01-SEP-2000; 2000WO-US24102.

XX 01-SEP-2000; 2000WO-US24102.

XX (EPTM-) EPIMUNE INC.

XX Grey HM, Sette A, Sidney J, Southwood S;

XX WPI; 2002-351766/38.

XX Immunogenic peptide with human leucocyte antigen-A2.1 binding site,
XX useful for treating e.g. viral infection or tumours -

XX Claim 1; Page 26; 35pp; English.

XX The invention describes a composition comprising an immunogenic peptide
XX having a human leucocyte antigen (HLA)-A2.1 binding site. The peptides
XX bind specifically to HLA-A2.1, to cause T cell activation and thus a
XX cytotoxic T cell response. The peptides and the nucleic acids that
XX encode them, are used, in vivo or ex vivo, for treatment of viral
XX infections (hepatitis B or C; Epstein-Barr; human immune deficiency;
XX Kaposi sarcoma; human papilloma; Lassa fever or cytomegalovirus);
XX tumours including prostate cancer, renal carcinoma and lymphoma (where
XX directed to prostate-specific antigen, p53, carcino-embryonal antigen,
XX Her2/neu or melanoma antigens); infection by Mycobacterium tuberculosis
XX or protozoa (directed to trypanosome surface antigen); and condyloma
XX acuminatum. The peptides are suitable for use in peptide-based
XX vaccines. This sequence represents an immunogenic peptide with the
XX human leucocyte antigen (HLA)-A2.1 binding site, described in the
XX invention.

XX Sequence 9 AA;

Query Match 20.0%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11

DB 4 RLIAF 8

RESULT 42

AAW01985

ID AAW01985 standard; peptide; 10 AA.

XX AAW01985;

XX

DT 26-SEP-1996 (first entry)

XX Peptide derived from hepatitis C virus NS4 protein.

us-09-441-061-2.rag

Thu Dec 19 17:47:38 2002

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XX Antigenic peptide; hepatitis C virus; HCV; non-A non-B;
KW non-structural protein 4; non-reactive; NS4;
KW
XX Hepatitis C virus.
OS
XX WO9604300-A1.
PN
XX 15-FEB-1996.
PD
XX 28-JUL-1995; 95WO-US09599.
PP
XX 29-JUL-1994; 94US-0282758.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH ) US SEC DEPT HEALTH.
PA
XX Fields HA, Khudyakov YE;
PI
XX PI; 1996-129330/13.
DF
XX Antigenic peptide(s) binding anti-hepatitis C virus antibodies -
PT useful for differential diagnosis of HCV in subjects
PT
XX Example; Page 29; 50pp; English.
PS
XX The present peptide, which was derived from the hepatitis C virus
CC (HCV) non-structural protein 4 (NS4), was prepd. using Fmoc
CC chemistry. It was tested for reactivity against a panel of 32
CC anti-HCV positive sera, and was found to react with none of them.
CC
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 3 RLIAF 7
RESULT 43
AAG96799
ID AAG96799 standard; Peptide; 10 AA.
AC AAG96799;
XX
XX 8-SEP-2001 (first entry)
DT
XX Human complementary peptide, SEQ ID NO: 2993.
DE
XX Human, complementary peptide; ligand; drug discovery; drug design.
KW
XX Homo sapiens.
OS
XX WO200142277-A2.
PN
XX 14-JUN-2001.
PD
XX 13-DEC-2000; 2000WO-GB04776.
PP
XX 13-DEC-1999; 99GB-0029464.
PR
XX (PROT-) PROTEOM LTD.
PA
XX Roberts GW, Heal JR;
PI
XX WPI; 2001-408419/43.
DR
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
PT

```

```

PT drug candidates or pro-drugs -
XX Example 4; Page 472; 646pp; English.
XX
XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ALPRL 8
DB 4 ALPRL 8
RESULT 44
AAJ01931
ID AAJ01931 standard; Peptide; 10 AA.
XX
XX AAJ01931;
AC
XX 02-JUL-2001 (first entry)
DT
XX Hepatitis C virus epitope #1922.
DE
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
KW
XX Hepatitis C virus.
OS
XX WO200121189-A1.
PN
XX 29-MAR-2001.
PD
XX 19-JUL-2000; 2000WO-US19774.
PP
XX 19-JUL-1999; 99US-0357737.
PR
XX (EPIM-) EPIMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R,
XX Baker DM, Celis E, Kubo RT, Grey HW;
PI
XX WPI; 2001-308046/32.
DR
XX A new composition useful as a vaccine against hepatitis C virus -
XX Disclosure; Page 148; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
XX Sequence 10 AA;
SQ
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 6 RLIAF 10

```

RESULT 45
AAJ02783
ID AAJ02783 standard; Peptide; 10 AA.
XX
AC AAJ02783;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #2774.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cellis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccine against hepatitis C virus -
PT Disclosure; Page 168; 214pp; English.
XX
PS The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ0010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
XX
SQ Sequence 10 AA;
Query Match 20.0%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 3 RLIAF 7
RESULT 46
AAW21218
ID AAW21218 standard; peptide; 11 AA.
XX
AC AAW21218;
XX
DT 29-JUL-1997 (first entry)
XX
DE Farnesyl synthetase derived signal oligopeptide #18.
XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rheus;
KW gonadoliben precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast WMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX

OS Homo sapiens.
XX
PN WO9519568-A1.
XX
PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US00575.
XX
PR 14-JAN-1994; 94US-0182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication
PT between protein(s)
XX
PS Claim 5; Page 26; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface
CC of the protein and are represented by the hydrophilicity maxima of
CC the protein. These peptides are enriched in charged amino acids
CC arranged with neutral spacer amino acids. The specific signal
CC character of these oligopeptides is determined by a characteristic
CC combination of conformation and charge within the signal sequence.
CC These oligopeptides may be used as vaccines in the treatment of
CC human disease, as competitive inhibitors to prevent or reduce the
CC metabolic action or interaction of a selected protein by blocking
CC its specific signal sequences, or as therapeutic agents to function
CC as feedback regulators to reduce synthesis rate of a selected protein.
CC These peptides may be modified by omitting one or more amino acids at
CC the N- and/or C-terminal, by substituting one or more amino acids
CC without consideration of charge and polarity, by substituting one or
CC more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
XX
XX Sequence 11 AA;
Query Match 20.0%; Score 5; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 FSLKK 22
DB 7 FSLKK 11
RESULT 47
AAJ00088
ID AAJ00088 standard; Peptide; 11 AA.
XX
AC AAJ00088;
XX
DT 02-JUL-2001 (first entry)
XX
DE Hepatitis C virus epitope #79.
XX
KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.
XX
OS Hepatitis C virus.
XX
PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US19774.
XX
PR 19-JUL-1999; 99US-0357737.
XX

XX PA (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 103; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 7 RLIAF 11
 RESULT 48
 AAJ00671
 ID AAJ00671 standard; Peptide; 11 AA.
 XX AC AAJ00671;
 XX DT 02-JUL-2001 (first entry)
 XX DE Hepatitis C virus epitope #662.
 XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.
 XX OS Hepatitis C virus.
 XX PN WO200121189-A1.
 XX PD 29-MAR-2001.
 XX PF 9-JUL-2000; 2000WO-US19774.
 XX PR 19-JUL-1999; 99US-0357737.
 XX PS (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX PD 29-MAR-2001.
 XX PF 9-JUL-2000; 2000WO-US19774.
 XX PR 19-JUL-1999; 99US-0357737.
 XX PS (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 117; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 7 RLIAF 11

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 6 RLIAF 10
 RESULT 49
 AAJ00826
 ID AAJ00826 standard; Peptide; 11 AA.
 XX AC AAJ00826;
 XX DT 02-JUL-2001 (first entry)
 XX DE Hepatitis C virus epitope #817.
 XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.
 XX OS Hepatitis C virus.
 XX PN WO200121189-A1.
 XX PD 29-MAR-2001.
 XX PF 19-JUL-2000; 2000WO-US19774.
 XX PR 19-JUL-1999; 99US-0357737.
 XX PS (EPIM-) EPIMMUNE INC.
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 XX PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX DR WPI; 2001-308046/32.
 XX A new composition useful as a vaccines against hepatitis C virus -
 XX Disclosure; Page 121; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX SQ Sequence 11 AA;
 XX Y Match 20.0%; Score 5; DB 22; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 RESULT 50
 AAJ00842
 ID AAJ00842 standard; Peptide; 11 AA.
 XX AC AAJ00842;
 XX DT 02-JUL-2001 (first entry)
 XX DE Hepatitis C virus epitope #833.
 XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX KW antiviral.
 XX OS Hepatitis C virus.

PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI PI Baker DM, Celis E, Kubo RT, Grey HW;
XX XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus
XX
XX Disclosure; Page 122; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11
RESULT 51
AAJ01943
ID AAJ01943 standard; Peptide; 11 AA.
XX
XX AAJ01943;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #1934.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI PI Baker DM, Celis E, Kubo RT, Grey HW;
XX XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus
XX
XX Disclosure; Page 148; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11

CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 7 RLIAF 11
RESULT 52
AAJ02021
ID AAJ02021 standard; Peptide; 11 AA.
XX
XX AAJ02021;
XX
XX 02-JUL-2001 (first entry)
XX
XX Hepatitis C virus epitope #2012.
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX WO200121189-A1.
XX
XX 29-MAR-2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX PF
XX 19-JUL-1999; 99US-0357737.
XX PR
XX (EPIM-) EPIMMUNE INC.
XX PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI PI Baker DM, Celis E, Kubo RT, Grey HW;
XX XX
XX WPI; 2001-308046/32.
XX
XX A new composition useful as a vaccines against hepatitis C virus
XX
XX Disclosure; Page 150; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 11 AA;
Query Match 20.0%; Score 5; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 6 RLIAF 10
RESULT 53
AAJ02097
ID AAJ02097 standard; Peptide; 11 AA.
XX
XX AAJ02097;
XX
XX 02-JUL-2001 (first entry)
XX

US-09-441-061-2.rag

Thu Dec 19 17:47:38 2002

DE Hepatitis C virus epitope #2088.
 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 PN 29-MAR-2001.
 PD 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XY WPI; 2001-308046/32.
 DE A new composition useful as a vaccine against hepatitis C virus -
 XX Disclosure; Page 152; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX Sequence 11 AA;
 SQ Query Match 20.0%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 1 RLIAF 5
 RESULT 55
 AAJ02600
 ID AAJ02600 standard; Peptide; 11 AA.
 XX AC AAJ02600;
 XX 02-JUL-2001 (first entry)
 DT Hepatitis C virus epitope #2591.
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX Hepatitis C virus.
 OS WO200121189-A1.
 PN 29-MAR-2001.
 PD 19-JUL-2000; 2000WO-US19774.
 XX 19-JUL-1999; 99US-0357737.
 PR (EPIM-) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 DE A new composition useful as a vaccine against hepatitis C virus -
 XX Disclosure; Page 164; 214pp; English.
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX Sequence 11 AA;
 SQ Query Match 20.0%; Score 5; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RLIAF 11
 DB 4 RLIAF 8
 Search completed: December 19, 2002, 17:43:06

us-09-441-061-2.rag

Thu Dec 19 17:47:38 2002

Job time : 35 secs

Thu Dec 19 17:47:44 2002

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 ; Search time 15 seconds
(without alignments)
160.224 Million cell updates/sec

Title: US-09-441-061-2
Perfect score: 25
Sequence: 1 GNAALPRLIAFTSEHSFLSKGAA 25

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0
Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database : PIR.73.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	20.0	25	H64710	hypothetical prote
2	4	16.0	8	XGHU8U	urine glycopeptide
3	4	16.0	10	PC2171	triacylglycerol li
4	4	16.0	15	PA0087	cytochrome c2 - fu
5	4	16.0	18	B48408	21K high mobility
6	4	16.0	18	S58277	insulin-like growt
7	4	16.0	20	S58277	insulin-like growt
8	4	16.0	22	A20527	arylsulfatase A -
9	3	12.0	5	JN0860	prostaglandin-endo
10	3	12.0	6	C22565	peptidyl-di-peptida
11	3	12.0	7	I48105	R-phycocerythrin be
12	3	12.0	7	S66442	dihydrofolate redu
13	3	12.0	8	A23967	glutathione S-tran
14	3	12.0	9	A24244	leucopyrrokinin - M
15	3	12.0	9	A44873	adipokinetic hormo
16	3	12.0	9	A26363	caldesmon - rabbit
17	3	12.0	9	A61620	cardioactive pepti
18	3	12.0	9	S39766	locustamytotropin I
19	3	12.0	9	S27233	cardioactive pepti
20	3	12.0	9	P02025	ig heavy chain CDR
21	3	12.0	9	A60427	macrophage cytotox
22	3	12.0	9	S78762	ribosomal protein
23	3	12.0	9	A33527	fructose-2,6-bisph
24	3	12.0	9	S39767	cardioactive pepti
25	3	12.0	9	PC7073	ubiquinol-cytochro
26	3	12.0	9	S15594	orf 1 rara 5'-regi
27	3	12.0	10	A60624	angiotensin I - Ja
28	3	12.0	10	C45474	thrombospondin 2 -
29	3	12.0	10	G60787	sperm-activating p

30	3	12.0	10	2	C60787	sperm-activating p
31	3	12.0	10	2	E60787	sperm-activating p
32	3	12.0	10	2	E60527	sperm-activating p
33	3	12.0	10	2	E39572	sperm-activating p
34	3	12.0	10	2	D60589	sperm-activating p
35	3	12.0	10	2	C60588	sperm-activating p
36	3	12.0	10	2	A60588	sperm-activating p
37	3	12.0	10	2	XGHU8U	erythrocyte membra
38	3	12.0	10	2	S70251	nitrogenase (EC 1.
39	3	12.0	10	2	C61440	polygalacturonase
40	3	12.0	10	2	D61440	hemoglobin, extrac
41	3	12.0	10	2	S65728	acetylcholinestera
42	3	12.0	10	2	A24196	angiotensin precu
43	3	12.0	10	2	A90917	probable trpEG lea
44	3	12.0	10	2	LFTWNE	probable antigen 5
45	3	12.0	11	2	E41476	wound-induced prote
46	3	12.0	11	2	S19775	hypothetical prote
47	3	12.0	11	4	S52252	locustamytotropin -
48	3	12.0	12	1	A43975	t-complex polypept
49	3	12.0	12	2	G49410	malate dehydrogena
50	3	12.0	12	2	PNO162	polysialoglycoprot
51	3	12.0	12	2	A28955	T-cell receptor al
52	3	12.0	12	2	PH1190	insulin-like growt
53	3	12.0	12	2	A60528	ig gamma-2b chain
54	3	12.0	12	2	C30503	T-cell receptor be
55	3	12.0	12	2	PH1481	lebetin 1 isoform
56	3	12.0	12	2	S71380	alpha-conotoxin GI
57	3	12.0	13	1	NTKN2G	glutathione peroxi
58	3	12.0	13	2	A38929	ribosomal protein
59	3	12.0	13	2	S20578	locustamytotropin I
60	3	12.0	13	2	B61620	hypothetical prote
61	3	12.0	13	2	S09395	polysialoglycoprot
62	3	12.0	13	2	B28955	hemolytic protein
63	3	12.0	13	2	S09019	ig heavy chain CRD
64	3	12.0	13	2	PT0290	conceptus protein
65	3	12.0	13	2	B61233	unidentified QM002
66	3	12.0	13	2	PN0048	H+-transporting tw
67	3	12.0	13	2	S01904	mastoparan - yello
68	3	12.0	14	1	QMVAVV	trp operon leader
69	3	12.0	14	1	QMVHVM	somatostatin I - c
70	3	12.0	14	1	LFEHWT	somatostatin I - c
71	3	12.0	14	2	C60414	somatostatin - spo
72	3	12.0	14	2	B60842	somatostatin I - E
73	3	12.0	14	2	A60622	somatostatin I - E
74	3	12.0	14	2	A60840	somatostatin I - s
75	3	12.0	14	2	S00172	somatostatin I - s

ALIGNMENTS

RESULT 1

H64710 Hypothetical protein HP1528 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: H64710

R:Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: H64710

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-25 <POM>

A:Cross-references: GB:AE000651; GB:AE000511; NID:92314708; PIDN:ARD08577.1; PID:9231471

Query Match 20.0%; Score 5; DB 2; Length 25;

Best Local Similarity 100.0%; Pred.No. 95;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Dec 19 17:47:44 2002

Query Match 16.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 21 KKGA 24
DB 6 KKGA 9

RESULT 5

B48408
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A03188
R:Lotz, C.J.; Weiss, J.B.
Biochem. J. 123, 25P, 1971
A:Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
A:Reference number: A03188; PMID:5126885
A:Accession: A03188
A:Molecule type: protein
A:Residues: 1-8 <LOT>
C:Keywords: glycoprotein
P:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 16.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGAA 25
DB 4 KGAA 7

RESULT 6

S58277
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C:Accession: S58277
R:Smrzka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.P.; Barlow, D.P.
submitted to the EMBL Data Library, January 1995
A:Description: Conservation of a methylation imprint and a putative imprinting box at
A:Reference number: S58277
A:Accession: S58277
A:Molecule type: DNA
A:Residues: 1-18 <SMR>
A:Cross-references: EMBL:X83702; NID:929644; PIDN:CAA58675.1; PID:9929645
C:Keywords: growth factor receptor

Query Match 16.0%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AALP 6
DB 9 AALP 12

RESULT 7

I54283
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I54283
R:Regis, S.; Carrozzio, R.; Filocamo, M.; Serra, G.; Mastropasolo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995
A:Title: An An-deletion causing a frameshift in the arylsulphatase A gene of a late inf
A:Reference number: I54283; PMID:95362256; PMID:7635478
A:Accession: I54283
A:Status: preliminary; translated from GB/EMBL/DDBJ

QY 19 SLKKG 23
DB 13 SLKKG 17

RESULT 2

XGHUEU
urine glycopeptide - human
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A03188
R:Lotz, C.J.; Weiss, J.B.
Biochem. J. 123, 25P, 1971
A:Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
A:Reference number: A03188; PMID:5126885
A:Accession: A03188
A:Molecule type: protein
A:Residues: 1-8 <LOT>
C:Keywords: glycoprotein
P:1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 16.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 EHSK 17
DB 2 EHSK 5

RESULT 3

PC2171
C:Species: Rhizopus niveus
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C:Accession: PC2171
R:Kohno, M.; Kugimura, Y.; Hashimoto, Y.; Morita, Y.
Biochim. Biophys. Acta 1107, 107-112, 1994
A:Title: Purification, characterization, and crystallization of two types of lipase from
A:Reference number: PC2171; PMID:94319059; PMID:7765029
A:Accession: PC2171
A:Molecule type: protein
A:Residues: 1-10 <KOH>
C:Keywords: This enzyme catalyzes the hydrolysis of the ester bonds.
C:Keywords: carboxylic ester hydrolase

Query Match 16.0%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AALP 6
DB 3 AALP 6

RESULT 4

PA0087
cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0087
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPIID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0087
A:Accession: PA0087
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: electron transfer; heme; photosynthesis

Thu Dec 19 17:47:44 2002

us-09-441-061-2.rpr

A/Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A/Reference number: A22565; MUID:85182601; PMID:3886644

A/Accession: C22565
 A/Molecule type: protein
 A/Residues: 1-6 <KLO>

Query Match 12.0%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MAA 4
 Db 1 MAA 3

RESULT 11

I48105
 A/Title: dihydrofolate reductase - Chinese hamster (fragment)
 C/Species: Crictetus griseus (Chinese hamster)
 C/Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C/Accession: I48105
 R/Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
 Biochemistry 25, 6228-6236, 1986

A/Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydr
 A/Reference number: I48105; MUID:87076541; PMID:3024702

A/Accession: I48105
 A/Molecule type: protein
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-7 <RES>
 A/Cross-references: GB:M14771; NID:G191055; PIDN:AAA36975.1; PID:G191056

Query Match 12.0%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LIA 10
 Db 5 LIA 7

RESULT 12

S66442
 A/Title: glutathione S-transferase P - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C/Accession: S66442
 R/Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.

Eur. J. Biochem. 232, 106-110, 1995

A/Title: Identification of the electrophilic substrate-binding site of glutat
 A/Reference number: S66442; MUID:96048035; PMID:7556138

A/Accession: S66442
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-7 <NIS>

Query Match 12.0%; Score 3; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ALP 6
 Db 1 ALP 3

RESULT 13

A23967
 A/Title: leucopyrokinin - Madeira cockroach

C/Species: Leucophaea maderae (Madeira cockroach)

C/Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 11-Jul-1997

C/Accession: A23967

R/Nachman, R.J.; Holman, G.M.; Cook, B.J.

Biochem. Biophys. Res. Commun. 137, 936-942, 1986

A/Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: structu

A/Molecule type: DNA

A/Residues: 1-20 <RES>

A/Cross-references: GB:878735; NID:G1037139; PIDN:AA335013.1; PID:G1037140

Query Match 16.0%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LPRL 8
 Db 11 LPRL 14

RESULT 8

A20527
 A/Title: prostaglandin-endoperoxide synthase (EC 1.14.99.1) - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon (domestic sheep)

C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 26-May-2000

C/Accession: A20527

R/Roth, G.J.; Machuga, E.T.; Ozols, J.

Biochemistry 22, 4672-4675, 1983

A/Title: Isolation and covalent structure of the aspirin-modified, active-site region of

A/Reference number: A20527; MUID:84024608; PMID:6414516

A/Accession: A20527

A/Molecule type: protein

A/Residues: 1-22 <ROT>

A/Superfamily: human prostaglandin-endoperoxide synthase; EGF homology

C/Keywords: oxidoreductase

Query Match 16.0%; Score 4; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 FSLK 21
 Db 7 FSLK 10

RESULT 9

JN0860
 A/Title: peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito

C/Species: Sarda orientalis (striped bonito)

C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C/Accession: JN0860

R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A/Reference number: JN0859; MUID:94080036; PMID:7764272

A/Accession: JN0860

A/Molecule type: protein

A/Residues: 1-5 <MAT>

A/Experimental source: intestine

C/Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin

C/Superfamily: bradykinin-potentiating peptide

C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 12.0%; Score 3; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ALP 6
 Db 1 ALP 3

RESULT 10

C22565
 A/Title: R-phycoerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)

C/Species: Gastrocloonium coulteri

C/Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C/Accession: C22565

R/Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Reference number: A23967; PMID:86269041; PMID:3015140

A;Accession: A23967

A;Molecule type: protein

A;Residues: 1-8 <NAC>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8

DB 6 PRL 8

RESULT 14

A24244

N;A; innatic hormone - bollworm

C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997

C;Accession: A24244

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio

A;Reference number: A24244; PMID:86186794; PMID:3964263

A;Accession: A24244

A;Molecule type: protein

A;Residues: 1-9 <VAP>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTS 13

DB 4 FTS 6

RESULT 15

A44873

ca; mon - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C;Accession: A44873

R;Ikeda, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by prote

A;Reference number: A44873; PMID:91378498; PMID:1898046

A;Accession: A44873

A;Molecule type: protein

A;Residues: 1-9 <KE>

A;Experimental source: skeletal myosin

A;Note: sequence extracted from NCBI backbone (NCBI:63199)

C;Superfamily: caldesmon

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21

DB 3 SLK 5

RESULT 16

A26363

cardioactive peptide - green crab (fragment)

C;Species: Carcinus maenas (green crab, common shore crab)

C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993

C;Accession: A26363

R;Scangier, J.; Hilbich, C.; Beyreuther, K.; Keller, R.

Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987

A;Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crat

A;Reference number: A26363

A;Accession: A26363

A;Molecule type: protein

A;Residues: 1-9 <STA>

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12

DB 5 APT 7

RESULT 17

A61620

locustamytropin III - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997

C;Accession: A61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A;Title: Isolation, identification and synthesis of locustamytropin III and IV, two a

A;Reference number: A61620

A;Accession: A61620

A;Molecule type: protein

A;Residues: 1-9 <SCH>

C;Keywords: amidated carboxyl end; neuropeptide

F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8

DB 7 PRL 9

RESULT 18

S39766

cardioactive peptide CCAP - yellow mealworm

C;Species: Tenebrio molitor (yellow mealworm)

C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999

C;Accession: S39766

R;Furuya, K.; Liao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A.

Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993

A;Title: Isolation and identification of a cardioactive peptide from Tenebrio molitor

A;Reference number: S39766; PMID:94176032; PMID:8129851

A;Accession: S39766

A;Molecule type: protein

A;Residues: 1-9 <FUR>

C;Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12

DB 5 APT 7

RESULT 19

S27233
cardioactive peptide CCAP - tobacco hornworm
C/Species: Manduca sexta (tobacco hornworm)
C/Date: 09-Jun-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C/Accession: S27233
R/Cheng, C.C.; Loi, P.K.; Sylwester, A.W.; Lee, T.D.; Tublitz, N.J.
FEBS Lett. 313, 165-168, 1992
A/Title: Primary structure of a cardioactive neuropeptide from the tobacco hawkmoth, *Manduca sexta*
A/Reference number: S27233; MUID:93050243; PMID:1426284
A/Accession: S27233
A/Molecule type: protein
A/Residues: 1-9 <CHE>
C/Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
|||
DB 5 APT 7

RESULT 20
PT0225
Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
A/Accession: PT0225
R/Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene usage in the development of the B cell repertoire
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0225
A/Molecule type: DNA
A/Residues: 1-9 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMA 3
|||
DB 5 GMA 7

RESULT 21
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C/Accession: A60427
R/Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A/Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducing factor, 29K
A/Reference number: A60427; MUID:91372335; PMID:1909970
A/Accession: A60427
A/Molecule type: protein
A/Residues: 1-9 <JON>
A/Note: the sequence from the text on page 706 is inconsistent with that from page 708
C/Keywords: cytokine

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
|||
DB 1 GAA 3

RESULT 22

S78762
ribosomal protein MRP-S12, mitochondrial - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: S78762
R/Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A/Reference number: S78760
A/Accession: S78762
A/Molecule type: protein
A/Residues: 1-9 <GRA>
C/Keywords: mitochondrial
P/1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
|||
DB 7 PRL 9

RESULT 23

A33527
fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - rat (fragment)
N/Alternate names: fructose-2,6-bisphosphatase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jun-1993
C/Accession: A33527
R/Kitamura, K.; Uyeda, K.; Hartman, P.C.; Kangawa, K.; Matsuo, H.
J. Biol. Chem. 264, 6344-6348, 1989
A/Title: Catalytic site of rat liver and bovine heart fructose-6-phosphate, 2-kinase:fructose-2,6-bisphosphate 2-phosphatase
A/Reference number: A33527; MUID:89197937; PMID:2539378
A/Accession: A33527
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <KIT>
C/Keywords: phosphoric monoester hydrolase

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAL 5
|||
DB 6 AAL 8

RESULT 24

S39767
cardioactive peptide CCAP - Spodoptera eridania
C/Species: Spodoptera eridania
C/Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
C/Accession: S39767
R/Furuya, K.; Liso, S.; Reynolds, S.B.; Ota, R.B.; Hackett, M.; Schooley, D.A.
Biochem. Biophys. Res. Commun. 193, 1065-1074, 1993
A/Title: Isolation and identification of a cardioactive peptide from *Tenebrio molitor* an
A/Reference number: S39766; MUID:94176032; PMID:8429851
A/Accession: S39767
A/Molecule type: protein
A/Residues: 1-9 <FUR>
C/Keywords: neuropeptide

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 APT 12
|||
DB 5 APT 7

Thu Dec 19 17:47:44 2002

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
PC7073
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Jun-2002
C:Accession: PC7073

R;Tsuji, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b
A:Reference number: PC7072
A:Accession: PC7073

A:Molecule type: protein
A:Residues: 1-9 <TSU>
C:Keywords: brain; core protein; oxidoreductase

Query Match 12.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
|||
DB 1 SLK 3

RESULT 26
S15594
orf 1 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15594
R;Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15594
A:Molecule type: DNA
A:Residues: 1-9 <BRA>
A:Cross-references: EMBL:X56057; NID:g35875
A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARAL, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics: S15594
A:Gene: GDB:RARA
A:Cross-references: GDB:120337; OMIM:180240
A:Map position: 17q12-17q12

Query Match 12.0%; Score 3; DB 4; Length 9;
Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAA 4
|||
DB 1 MAA 3

RESULT 27
A60624
angiotensin I - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C:Accession: A60624
R;Takei, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of the
A:Reference number: A60624; MUID:90284684; PMID:2191893
A:Accession: A60624
A:Molecule type: protein
A:Residues: 1-10 <TAK>
A:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;

QY 18 FSL 20
|||
DB 8 FSL 10

RESULT 28
C45474
thrombospondin 2 - bovine (fragment)
N;Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homol
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Aug-1998
C:Accession: C45474
R;Pellerin, S.; Lafeuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; F
J. Biol. Chem. 268, 4304-4310, 1993
A:Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by a
A:Reference number: A45474; MUID:93179438; PMID:8382699
A:Accession: C45474
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <PEL>
A:Experimental source: adrenocortical cells
A:Note: Sequence extracted from NCBI backbone (NCBIP:125844)
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology;

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
|||
DB 8 SLK 10

RESULT 29
G60787
sperm-activating peptide (Ser-3,5,7 speract) - sea urchin (Anthocidaris crassispina).
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: G60787
R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka,
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: G60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all o
at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
|||
DB 2 FSL 4

RESULT 30
C60787
sperm-activating peptide (Ser-3,10 speract) - sea urchin (Hemicentrotus pulcherrimus)
C:Species: Hemicentrotus pulcherrimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: C60787
R;Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka,
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: C60787
A:Molecule type: protein

Thu Dec 19 17:47:44 2002

us-09-441-061-2.rpt

A:Residues: 1-10 <SUZ>
 C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 31

E60787 sperm-activating peptide (Ser-3,5,7, Asp-10 speract) - sea urchin (Hemicentrotus pulcherrimus)
 C:Species: Hemicentrotus pulcherrimus
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000

C:Accession: E60787
 R:Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.

Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus

A:Reference number: A60787; PMID:88242184; PMID:3378407
 A:Accession: E60787

A:Molecule type: protein

A:Residues: 1-10 <SUZ>

C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.
 C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 32

E60527 sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)
 N:Alternate names: speract homolog TG-7

C:Species: Tripneustes gratilla
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C:Accession: E60527; G39572
 R:Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
 A:Reference number: A60527

A:Accession: E60527

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Note: this peptide did not contain bromophenylalanine

R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991
 A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate

A:Reference number: A39572; PMID:91283461; PMID:2059627
 A:Accession: G39572

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Note: this peptide contained bromophenylalanine

C:Superfamily: unassigned animal peptides

F:2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20

Db 2 FSL 4
 ||||

RESULT 33

E39572 sperm-activating peptide TG-5 - sea urchin (Tripneustes gratilla)

N:Alternate names: speract homolog TG-5

C:Species: Tripneustes gratilla

C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000

C:Accession: E39572

R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991

A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate

A:Reference number: A39572; PMID:91283461; PMID:2059627

A:Accession: E39572

A:Molecule type: protein

A:Residues: 1-10 <YOS>

C:Superfamily: unassigned animal peptides

F:2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||

Db 2 FSL 4

RESULT 34

D60589 sperm-activating peptide (Ser-3,5 SAP-I) - Echinometra mathaei

C:Species: Echinometra mathaei

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C:Accession: D60589

R:Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989

A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527

A:Accession: D60589

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Note: an identical peptide was isolated from Echinometra mathaei type A and type B

C:Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||

Db 2 FSL 4

RESULT 35

C60588 sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)

N:Alternate names: speract homolog

C:Species: Strongylocentrotus nudus

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C:Accession: C60588

R:Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989

A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.

A:Reference number: A60527

A:Accession: C60588

A:Molecule type: protein

A:Residues: 1-10 <YOS>

C:Superfamily: unassigned animal peptides

Thu Dec 19 17:47:44 2002

regions as part of the nif1/2 gene clusters.

A;Reference number: S70242; MUID:96296457; PMID:8709854
 A;Accession: S70251
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-10 <SCH>
 A;Cross-references: EMBL:U25160; NID:g1160347; PIDN:AAC43540.1; PID:g1160348
 A;Experimental source: ATCC 29413
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C;Genetics:
 A;Gene: nifH2
 C;Keywords: ATP; iron-sulfur protein; nitrogen fixation; oxido-reductase

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IAF 11
 ||||
 Db 8 IAF 10

RESULT 39

C61440
 polygalacturonase (EC 3.2.1.15) II b - Aspergillus sp. (fragment)
 C;Species: Aspergillus sp.
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
 C;Accession: C61440
 R;Stratillova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jorvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A;Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and st
 A;Reference number: A61440; MUID:93151962; PMID:8427629
 A;Accession: C61440
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STR>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFT 12
 ||||
 Db 4 AFT 6

RESULT 40

D61440
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C;Species: Aspergillus sp.
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996
 C;Accession: D61440
 R;Stratillova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jorvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A;Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and st
 A;Reference number: A61440; MUID:93151962; PMID:8427629
 A;Accession: D61440
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STR>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PTS 13
 ||||
 Db 5 PTS 7

RESULT 41

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 36

A60588
 sperm-activating peptide (Ser-3,5 SAP-I) - sea urchin (Strongylocentrotus nudus)
 A;Alternate names: speract homolog
 C;Species: Strongylocentrotus nudus
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C;Accession: A60588
 R;Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, T.;
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A; e: A halogenated amino acid-containing sperm activating peptide and its related pe
 ot, nudus, Echinometra mathaei and Heterocentrotus mamillatus.
 A;Reference number: A60527

A;Accession: A60588
 A;Molecule type: protein
 A;Residues: 1-10 <YOS>
 C;Superfamily: unassigned animal peptides

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
 ||||
 Db 2 FSL 4

RESULT 37

XGHUE
 erythrocyte membrane glycopeptide - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: A03187
 R;Weiss, J.B.; Lote, C.J.; Bobinski, H.
 Nature New Biol. 234, 25-26, 1971
 A;Title: New low molecular weight glycopeptide containing triglucoylcysteine in human e
 A;Reference number: A03187; MUID:72034940; PMID:5286858

A;Accession: A03187
 A;Molecule type: protein
 A;Residues: 1-10 <WEI>
 C;Comment: The identity of the glycoprotein from which this peptide is derived is unknown
 found (see PIR:XGHUE)
 C;Superfamily: unassigned animal peptides
 C;Keywords: glycoprotein
 F;Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 12.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 HSH 17
 ||||
 Db 4 HSH 6

RESULT 38

S70251
 nitrogenase (EC 1.18.6.1) iron protein - Anabaena variabilis (fragment)

C;Species: Anabaena variabilis
 C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 19-Jan-2001
 C;Accession: S70251
 R;Schrautemeier, B.; Neveling, U.; Schmitz, S.
 Mol. Microbiol. 18, 357-369, 1995
 A;Title: Distinct and differentially regulated Mo-dependent nitrogen-fixing systems evolved

Thu Dec 19 17:47:44 2002

us-09-441-061-2.tpr

```

865728
hemoglobin, extracellular, chain di - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65728
R:Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721, MUID:96176855, PMID:8597573
A:Accession: S65728
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <FUS>

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
DB 7 SLK 9

RESULT 42
A24196
acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)
C:Species: Electrophorus electricus (electric eel)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Apr-1993
C:Accession: A24196
R:Kieffer, B.; Goeldner, M.; Hirth, C.; Aebersold, R.; Chang, J.Y.
FEBS Lett. 202, 91-96, 1986
A:Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase
A:Reference number: A24196
A:Accession: A24196
A:Molecule type: protein
A:Residues: 1-10 <KIE>
C:Keywords: carboxylic ester hydrolase

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 43
A90917
angiotensin precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90917, A01250
R:Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A:Reference number: A90917, MUID:74127845, PMID:4361802
A:Accession: A90917
A:Molecule type: protein
A:Residues: 1-10 <NAK>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
DB 8 FSL 10

865728
hemoglobin, extracellular, chain di - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65728
R:Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721, MUID:96176855, PMID:8597573
A:Accession: S65728
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <FUS>

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLK 21
DB 7 SLK 9

RESULT 42
A24196
acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)
C:Species: Electrophorus electricus (electric eel)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Apr-1993
C:Accession: A24196
R:Kieffer, B.; Goeldner, M.; Hirth, C.; Aebersold, R.; Chang, J.Y.
FEBS Lett. 202, 91-96, 1986
A:Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase
A:Reference number: A24196
A:Accession: A24196
A:Molecule type: protein
A:Residues: 1-10 <KIE>
C:Keywords: carboxylic ester hydrolase

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 43
A90917
angiotensin precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90917, A01250
R:Nakayama, T.; Nakajima, T.; Sokabe, H.
Chem. Pharm. Bull. 21, 2085-2087, 1973
A:Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
A:Reference number: A90917, MUID:74127845, PMID:4361802
A:Accession: A90917
A:Molecule type: protein
A:Residues: 1-10 <NAK>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 12.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 FSL 20
DB 8 FSL 10

```

```

RESULT 44
LFTWE
probable trpEG leader peptide - Thermus aquaticus
C:Species: Thermus aquaticus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C:Accession: S03315
R:Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A:Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and
A:Reference number: S03315, MUID:89000781, PMID:2844259
A:Accession: S03315
A:Molecule type: DNA
A:Residues: 1-11 <SAT>
A:Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30565.1; PID:948262
A>Note: the source is designated as Thermus thermophilus HB8
C:Genetics:
A:Gene: trpL
C:Superfamily: probable trpEG leader peptide

Query Match 12.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALP 6
DB 2 ALP 4

RESULT 45
E41476
probable antigen 5 - Mycobacterium leprae (fragment)
C:Species: Mycobacterium leprae
C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993
R:Hartseer, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.
Infect. Immun. 58, 2821-2827, 1990
A:Title: Selection and characterization of recombinant clones that produce Mycobacterium
A:Reference number: A41476; MUID:90354041; PMID:1696931
A:Accession: E41476
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <HAR>

Query Match 12.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPR 7
DB 4 LPR 6

RESULT 46
S19775
wound-induced protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C:Accession: S19775
R:Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A:Reference number: S19773
A:Accession: S19775
A:Molecule type: mRNA
A:Residues: 1-11 <PAR>
A:Cross-references: EMBL:X59884; NID:919323; PID:919324

Query Match 12.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 23
DB 5 KKG 7

```

A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <ROM>
A/Experimental source: reticulocyte
C/Superfamily: molecular chaperone t-complex-type

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LFA 10
DB 2 LFA 4

RESULT 50
PN0162
malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)
C/Species: Fusarium sporotrichioides
C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C/Accession: PN0162
R/Fukaya, N.; Chow, L.P.; Sugita, Y.; Tugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A/Reference number: PN0160
A/Accession: PN0162
A/Molecule type: protein
A/Residues: 1-12 <FUK>
C/Keywords: oxidoreductase

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 51
A28955
polysialoglycoprotein repeating unit - whitespotted char
C/Species: Salvelinus leucomaenis pluvius (whitespotted char)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-1993
C/Accession: A28955
R/Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.
Biochemistry 27, 7141-7145, 1988
A/Title: Comparative structures of the polysialoglycoproteins from unfertilized and fertilized oocytes of the Japanese medaka, *Oryzias latipes*
A/Reference number: A90537; MUID:89062454; PMID:3196707
A/Accession: A28955
A/Molecule type: protein
A/Residues: 1-12 <KIT>
C/Keywords: glycoprotein

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TSE 14
DB 4 TSE 6

RESULT 52
PH1190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1190
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor peptide
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: S26512

A>Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <ROM>
A/Experimental source: reticulocyte
C/Superfamily: molecular chaperone t-complex-type

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LFA 10
DB 2 LFA 4

RESULT 50
PN0162
malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment)
C/Species: Fusarium sporotrichioides
C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C/Accession: PN0162
R/Fukaya, N.; Chow, L.P.; Sugita, Y.; Tugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A/Reference number: PN0160
A/Accession: PN0162
A/Molecule type: protein
A/Residues: 1-12 <FUK>
C/Keywords: oxidoreductase

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
DB 7 GAA 9

RESULT 51
A28955
polysialoglycoprotein repeating unit - whitespotted char
C/Species: Salvelinus leucomaenis pluvius (whitespotted char)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 31-Dec-1993
C/Accession: A28955
R/Kitajima, K.; Sorimachi, H.; Inoue, S.; Inoue, Y.
Biochemistry 27, 7141-7145, 1988
A/Title: Comparative structures of the polysialoglycoproteins from unfertilized and fertilized oocytes of the Japanese medaka, *Oryzias latipes*
A/Reference number: A90537; MUID:89062454; PMID:3196707
A/Accession: A28955
A/Molecule type: protein
A/Residues: 1-12 <KIT>
C/Keywords: glycoprotein

Query Match 12.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TSE 14
DB 4 TSE 6

RESULT 52
PH1190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1190
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor peptide
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: S26512

US-09-441-061-2.rpr

Thu Dec 19 17:47:44 2002

A/Accession: PH1481
 A/Molecule type: mRNA
 A/Residues: 1-12 <CAS>
 A/Experimental source: cytolytic T-lymphocyte
 A/Note: the authors translated the codon GGT for residue 2 as Ala and GCT for residue 3
 C/Superfamily: immunoglobulin homology
 C/Keywords: receptor; T-cell

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GAA 25
 |||
 Db 2 GAA 4

Search completed: December 19, 2002, 17:44:02
 Job time : 16 secs

A/Accession: PH190
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-12 <CAS>

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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SEH 15
 |||
 Db 4 SEH 6

RESULT 53
 A60528
 insulin-like growth factor-binding protein, serum - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
 C/Accession: A60528
 R/Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D.
 Comp. Biochem. Physiol. B 92, 561-567, 1989
 A/Title: Purification of the serum acid-stable insulin-like growth factor binding protein
 A/Reference number: A60528; MUID:89209787; PMID:2468442
 A/Accession: A60528
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <WAL>

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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGA 24
 |||
 Db 2 KGA 4

RESULT 54
 C30503
 IG gamma-2b chain C region (F5.5.1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
 C/Accession: C30503
 R/Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.
 J. Immunol. 141, 1754-1761, 1988
 A/Title: DNA rearrangements affecting both variable and constant regions of Ig H chain
 A/Reference number: A30503; MUID:88315788; PMID:2842402
 A/Accession: C30503
 A/Molecule type: mRNA
 A/Residues: 1-12 <GIL>
 A/Experimental source: myeloma cell line
 C/Keywords: immunoglobulin

Query Match 12.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRL 8
 |||
 Db 10 PRL 12

RESULT 55
 PH1481
 T-cell receptor beta chain (clone A24/PEG2) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C/Accession: PH1481
 R/Casanova, J.L.; Martinon, P.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
 J. Exp. Med. 177, 811-820, 1993
 A/Title: T cell receptor selection by and recognition of two class I major histocompatib
 A/Reference number: PH1430; MUID:93171821; PMID:8436911

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 17:42:06 / Search time 14 Seconds
(without alignments)
52.541 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25

Sequence: 1 GMAALPRLIAFTSEHSHFLKGGAA 25

Scoring table: OLIGO Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size: 0

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Listing first 75 summaries

Database: Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	64.0	20	2	US-08-484-530-32
2	16	64.0	20	2	US-08-827-618A-32
3	16	64.0	20	3	US-08-483-952A-32
4	16	64.0	20	4	US-08-476-501-32
5	14	56.0	20	2	US-08-484-530-31
6	14	56.0	20	2	US-08-827-618A-31
7	14	56.0	20	3	US-08-483-952A-31
8	14	56.0	20	4	US-08-476-501-31
9	8	32.0	8	6	5475086-14
10	8	32.0	24	1	US-08-485-718-2
11	8	32.0	24	2	US-08-484-530-2
12	8	32.0	24	2	US-08-827-618A-2
13	8	32.0	24	3	US-08-483-952A-2
14	8	32.0	24	4	US-08-476-501-2
15	6	24.0	19	2	US-08-764-640-164
16	6	24.0	19	3	US-08-973-225-164
17	6	24.0	19	3	US-09-244-298A-164
18	6	24.0	19	4	US-09-516-704-164
19	6	24.0	19	4	US-09-549-090-164
20	5	20.0	10	1	US-08-282-758B-6
21	5	20.0	12	2	US-08-934-222-46
22	5	20.0	12	2	US-08-933-402-46
23	5	20.0	12	2	US-09-207-621-46
24	5	20.0	12	2	US-08-532-818-46
25	5	20.0	12	3	US-09-231-797-46
26	5	20.0	12	3	US-08-934-224-46
27	5	20.0	12	3	US-08-933-843-46

RESULT 1

US-08-484-530-32
Sequence 32, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

ALIGNMENTS

28	5	20.0	12	4	US-08-934-223-46	Sequence 46, Appl
29	5	20.0	12	4	US-09-413-492-46	Sequence 46, Appl
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31	5	20.0	15	4	US-09-009-953-184	Sequence 184, App
32	5	20.0	15	4	US-09-009-953-258	Sequence 258, App
33	5	20.0	18	4	US-09-109-957-11	Sequence 11, Appl
34	5	20.0	20	1	US-08-282-758B-2	Sequence 2, Appl
35	5	20.0	21	4	US-09-143-124-22	Sequence 22, Appl
36	5	20.0	21	4	US-09-009-953-206	Sequence 206, App
37	5	20.0	21	4	US-09-556-605-70	Sequence 70, Appl
38	5	20.0	21	4	US-09-556-605-73	Sequence 73, Appl
39	5	20.0	21	5	PCT-US92-07865-2	Sequence 2, Appl
40	5	20.0	22	2	US-08-146-028-58	Sequence 58, Appl
41	5	20.0	22	4	US-08-723-425A-58	Sequence 58, Appl
42	5	20.0	22	4	US-09-112-206-58	Sequence 58, Appl
43	5	20.0	23	6	5475086-9	Patent No. 5475086
44	5	20.0	24	3	US-08-592-500-36	Sequence 36, Appl
45	5	20.0	24	3	US-08-195-006-36	Sequence 36, Appl
46	5	20.0	24	5	PCT-US92-07865-3	Sequence 3, Appl
47	5	20.0	24	5	PCT-US94-07644A-36	Sequence 36, Appl
48	5	20.0	25	2	US-08-452-242-1	Sequence 1, Appl
49	5	20.0	25	2	US-08-934-741A-23	Sequence 23, Appl
50	5	20.0	25	3	US-08-453-176A-1	Sequence 1, Appl
51	5	20.0	25	3	US-08-451-374-1	Sequence 1, Appl
52	5	20.0	25	4	US-08-935-268A-1	Sequence 1, Appl
53	5	20.0	25	4	US-08-452-229-1	Sequence 2, Appl
54	4	16.0	6	1	US-08-785-247-6	Sequence 6, Appl
55	4	16.0	6	1	US-08-484-192-2	Sequence 2, Appl
56	4	16.0	6	3	US-08-798-394-2	Sequence 2, Appl
57	4	16.0	6	4	US-09-215-775-2	Sequence 2, Appl
58	4	16.0	7	4	US-09-370-644B-20	Sequence 20, Appl
59	4	16.0	8	4	US-08-953-033-19	Sequence 19, Appl
60	4	16.0	8	4	US-08-988-842-49	Sequence 49, Appl
61	4	16.0	9	1	US-07-942-245-504	Sequence 504, App
62	4	16.0	9	2	US-08-705-660-3	Sequence 3, Appl
63	4	16.0	9	2	US-08-350-260A-479	Sequence 479, App
64	4	16.0	9	3	US-08-989-045-3	Sequence 3, Appl
65	4	16.0	9	3	US-08-471-546-1	Sequence 1, Appl
66	4	16.0	9	3	US-08-159-339A-978	Sequence 978, App
67	4	16.0	9	3	US-08-471-586-6	Sequence 6, Appl
68	4	16.0	9	4	US-08-482-918-69	Sequence 69, Appl
69	4	16.0	9	4	US-09-224-681-69	Sequence 69, Appl
70	4	16.0	9	4	US-08-336-728A-69	Sequence 69, Appl
71	4	16.0	10	1	US-08-166-195A-38	Sequence 38, Appl
72	4	16.0	10	1	US-08-166-195A-39	Sequence 39, Appl
73	4	16.0	10	1	US-08-166-195A-40	Sequence 40, Appl
74	4	16.0	10	1	US-08-346-333-62	Sequence 62, Appl
75	4	16.0	10	2	US-08-436-772-38	Sequence 38, Appl

Query Match 64.0%; Score 16; DB 3; Length 20;

RESULT 2
US-08-827-618A-32
Sequence 32, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J
APPLICANT: Erlander, Mark G
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Irecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249

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Thu Dec 19 17:47:39 2002

```

Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFSLKKGAA 25
DB 1 AFTSEHSHFSLKKGAA 16

RESULT 4
US-08-476-501-32
Sequence 32, Application US/08476501
Patent No. 6455267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-32
Query Match 64.0%; Score 16; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AFTSEHSHFSLKKGAA 25
DB 1 AFTSEHSHFSLKKGAA 16

RESULT 5
US-08-484-530-31
Sequence 31, Application US/08484530
Patent No. 5846740
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:

```

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STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,530
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Irecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-530-31
Query Match 56.0%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAPTSE 14
DB 7 GMAALPRLIAPTSE 20

RESULT 6
US-08-827-618A-31
Sequence 31, Application US/08827618A
Patent No. 5998366
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: Erlander, Mark G.
APPLICANT: Kaufman, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,618A
FILING DATE: 09-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,725
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
ATTORNEY/AGENT INFORMATION:

```

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-952A-31

Query Match 56.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 8

US-08-476-501-31
Sequence 31, Application US/08476501
Patent No. 6455267
GENERAL INFORMATION:
APPLICANT: TOBIN, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,501
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A60780-10/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-501-31

Query Match 56.0%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 9

5475086-14
Patent No. 5475086
APPLICANT: TOBIN, ALLAN J.; ERLANDER, MARK G.; KAUFMAN,
DANIEL L.; CLARE-SALZLER, MICHAEL J.
TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
NUMBER OF SEQUENCES: 14

NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-12/RFT/NTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-618A-31

Query Match 56.0%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSE 14
DB 7 GMAALPRLIAFTSE 20

RESULT 7

US-08-483-952A-31
Sequence 31, Application US/08483952A
Patent No. 601139
GENERAL INFORMATION:
APPLICANT: Tobin, Allan J.
APPLICANT: ERLANDER, Mark G.
APPLICANT: KAUFMAN, Daniel L.
TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,952A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/716,909
FILING DATE: 18-JUN-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/586,536
FILING DATE: 21-SEP-1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-60780-7/RFT/NTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid

US-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/135,849
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 716,909
; FILING DATE: 18-JUN-1991
; APPLICATION NUMBER: 586,536
; FILING DATE: 21-SEP-1990
; SEQ ID NO:14:
; LENGTH: 8
5475086-14

Query Match          32.0%; Score 8; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 1 GMAALPRL 8

RESULT 10
US-08-485-718-2
; Sequence 2, Application US/08485718
; Patent No. 5705626
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J. G.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,718
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A60780-6/BIR
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-718-2

Query Match          32.0%; Score 8; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 11
US-08-484-530-2
; Sequence 2, Application US/08484530
; Patent No. 5846740
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,530
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard P.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-530-2

Query Match          32.0%; Score 8; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GMAALPRL 8
Db 17 GMAALPRL 24

RESULT 12
US-08-827-618A-2
; Sequence 2, Application US/08827618A
; Patent No. 5998366
; GENERAL INFORMATION:
; APPLICANT: Tobin, Allan J
; APPLICANT: Erlander, Mark G.
; APPLICANT: Kaufman, Daniel L.
; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

QY 1 GMAALPRL 8
 Db 17 GMAALPRL 24

RESULT 15
 US-08-764-640-164
 ; Sequence 164, Application US/08764640
 ; Patent No. 5869451
 ; Patent No. 5869451 5837683
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwirla, Steven E.
 ; APPLICANT: Gates, Christian
 ; APPLICANT: Schatz, Peter J.
 ; APPLICANT: Balasubramanian, Palaniappan
 ; APPLICANT: Wagstrom, Christopher R.
 ; APPLICANT: Hendren, Richard W.
 ; APPLICANT: Deprince, Randolph B.
 ; APPLICANT: Poddaturi, Surekha
 ; APPLICANT: Yin, Qun
 ; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 ; TITLE OF INVENTION: RECEPTOR
 ; NUMBER OF SEQUENCES: 244
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Glaxo Wellcome
 ; STREET: Five Moore Drive, P.O. Box 13398
 ; CITY: Research Triangle Park
 ; STATE: NC
 ; COUNTRY: USA
 ; ZIP: 27709
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/764,640
 ; FILING DATE: 11-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hrubic, Robert T.
 ; REGISTRATION NUMBER: 36,392
 ; REFERENCE/DOCKET NUMBER: PK3281
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-248-1000
 ; INFORMATION FOR SEQ ID NO: 164:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: linear
 ; TOPOLOGY: peptide
 ; MOLECULE TYPE: peptide
 ; US-08-764-640-164

Query Match 24.0%; Score 6; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
 Db 10 LKKGAA 15

RESULT 16
 US-08-973-225-164
 ; Sequence 164, Application US/08973225A
 ; Patent No. 6083913
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwirla, Steven E.

Duffin, David J.
 Gates, Christian
 Haselden, Sherril S.
 Mattheakis, Larry C.
 Schatz, Peter J.
 Wagstrom, Christopher R.
 Wrighton, Nicholas C.
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 ; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/973,225A
 FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubic, Robert T.
 REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 164:
 SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

TOPOLOGY: linear
 MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 164:
 US-08-973-225-164

Query Match 24.0%; Score 6; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
 Db 10 LKKGAA 15

RESULT 17
 US-09-244-298A-164
 ; Sequence 164, Application US/09244298A
 ; Patent No. 6121238
 ; GENERAL INFORMATION:
 ; APPLICANT: Dower, William J.
 ; APPLICANT: Barrett, Ronald W.
 ; APPLICANT: Cwirla, Steven E.
 ; APPLICANT: Gates, Christian
 ; APPLICANT: Schatz, Peter J.
 ; APPLICANT: Balasubramanian, Palaniappan
 ; APPLICANT: Wagstrom, Christopher R.
 ; APPLICANT: Hendren, Richard W.
 ; APPLICANT: Deprince, Randolph B.
 ; APPLICANT: Poddaturi, Surekha
 ; APPLICANT: Yin, Qun
 ; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 ; TITLE OF INVENTION: RECEPTOR

NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park

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Thu Dec 19 17:47:39 2002

REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-516-704-164
Query Match 24.0%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 LKKGAA 25
Db 10 LKKGAA 15
RESULT 19
US-09-549-090-164
Sequence 164, Application US/09549090
Patent No. 6465430
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwiria, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/973,225
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-549-090-164

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-164
Query Match 24.0%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 LKKGAA 25
Db 10 LKKGAA 15
RESULT 18
US-09-516-704-164
Sequence 164, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwiria, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Poduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

Query Match 24.0%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LKKGAA 25
Db 10 LKKGAA 15

RESULT 20
US-08-282-758B-6
Sequence 6, Application US/08282758B
Patent No. 5670310
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Differential Diagnosis of Chronic and Acute Hepatitis C
TITLE OF INVENTION: Virus Infection
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-282-758B-6

Query Match 20.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
Db 3 RLIAF 7

RESULT 21
US-08-934-222-46
Sequence 46, Application US/08934222
Patent No. 5928896
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

QY 3 AALPR 7
Db 7 AALPR 11

RESULT 22
US-08-933-402-46
Sequence 46, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
APPLICATION NUMBER: U.S. 08/051,741
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-46

Query Match 20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
Db 7 AALPR 11

RESULT 22
US-08-933-402-46
Sequence 46, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:

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Thu Dec 19 17:47:39 2002

```
US-09-207-621-46
Query Match      20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

RESULT 24
US-08-532-818-46
Sequence 46, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interactio
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIORITY APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-46

Query Match      20.0%; Score 5; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AALPR 7
Db 7 AALPR 11

RESULT 25
US-09-231-797-46
Sequence 46, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
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us-09-441-061-2-rai

Thu Dec 19 17:47:39 2002

TITLE OF INVENTION: Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/231,797
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 21-APR-1994
APPLICATION NUMBER: PCT/US94/04294
PRIOR APPLICATION DATA: U.S. 08/143,364
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-46

Query Match 20.0%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
DB 7 AALPR 11

RESULT 26
US-08-934-224-46
Sequence 46, Application US/08934224
Patent No. 610044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-46

Query Match 20.0%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
DB 7 AALPR 11

APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA: 08/532,818
APPLICATION NUMBER:
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA: U.S. 08/143,364
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-46

Query Match 20.0%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
DB 7 AALPR 11

RESULT 27
US-08-933-843-46
Sequence 46, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-SEPT-1997
APPLICATION NUMBER: US/08/933,843
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: 08/532,818
FILING DATE: 29-OCT-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-46

Query Match 20.0%; Score 5; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
DB 7 AALPR 11

us-09-441-061-2.rai

Thu Dec 19 17:47:39 2002

```
US-09-413-492-46
; Sequence 46, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interacti
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-413-492-46
Query Match 20.0%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AALPR 7
DB 7 AALPR 11
RESULT 30
US-09-009-953-173
; Sequence 173, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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RESULT 29

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 184:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 184:

US-09-009-953-184

Query Match 20.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11

Db 6 RLIAF 10

RESULT 32

US-09-009-953-258

; Sequence 258, Application US/09009953

; Patent No. 6413517

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; REACTIVE DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION NUMBER: US/09/009,953

; FILING DATE: 21-Jan-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,713

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/037,432

; FILING DATE: 07-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-011520US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 258:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 258:

US-09-009-953-258

Query Match

20.0%; Score 5; DB 4; Length 15;

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 173:

US-09-009-953-173

Query Match 20.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11

Db 7 RLIAF 11

RESULT 31

US-09-009-953-184

; Sequence 184, Application US/09009953

; Patent No. 6413517

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; TITLE OF INVENTION: Identification of Broadly

; REACTIVE DR Restricted Epitopes

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,953

; FILING DATE: 21-Jan-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/036,713

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/037,432

; FILING DATE: 07-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

```
TELEFAX: (404) 818-3799
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-282-758B-2

Query Match 20.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
DB 3 RLIAF 7

RESULT 35
US-09-143-124-22
; Sequence 22, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-22

Query Match 20.0%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
DB 12 KKGAA 16

RESULT 36
US-09-009-953-206
; Sequence 206, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; REACTIVE DR RESTRICTED EPITOPES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

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ORIGINAL SOURCE: Hepatitis C Virus
ORGANISM: DP2, amino acids 1902 to 1922 of
INDIVIDUAL ISOLATE: HCV polyprotein
INDIVIDUAL ISOLATE: HCV polyprotein
PCT-US92-07865-2
Query Match 20.0%; Score 5; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 91; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 7 RLIAF 11
Db 17 RLIAF 21

RESULT 40
US-08-146-028-58
US-08-146-028-58 Application US/08146028
Sequence 58, Patent No. 5891640
GENERAL INFORMATION:
APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/08/146,028
APPLICATION FOR SEQ ID NO: 58;
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE: HCV
INDIVIDUAL ISOLATE: HCV
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
NAME/KEY: Modified-site
LOCATION: 22
US-08-146-028-58
Query Match 20.0%; Score 5; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 95; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 7 RLIAF 11
Db 11 RLIAF 15

RESULT 41
US-08-723-425A-58
US-08-723-425A-58 Application US/08723425A
Sequence 58, Patent No. 6185730
GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 453
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE, P.C.

```

```

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/723,425A
APPLICATION NUMBER: US/08/723,425A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 58;
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE: HCV
INDIVIDUAL ISOLATE: HCV
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
NAME/KEY: Modified-site
LOCATION: 22
US-08-723-425A-58
Query Match 20.0%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 95; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 7 RLIAF 11
Db 11 RLIAF 15

RESULT 42
US-09-112-206-58
US-09-112-206-58 Application US/09112206
Sequence 58, Patent No. 6210903
GENERAL INFORMATION:
APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/09/112,206
APPLICATION NUMBER: US/09/112,206
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,028
FILING DATE:
INFORMATION FOR SEQ ID NO: 58;
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids

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us-09-441-061-2.ra1

Thu Dec.19 17:47:39 2002

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE: HCV
INDIVIDUAL ISOLATE:
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 22
US-09-112-206-58
Query Match 20.0%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RLIAF 11
DB 11 RLIAF 15
RESULT 43
5475086-9
PATENT NO. 5475086
APPLICANT: TOBIN, ALLAN J.;ERLANDER, MARK G.;KAUFMAN,
DANIEL L.;CLARE-SALZLER, MICHAEL J.
TITLE OF INVENTION: CLONED GLUTAMIC ACID DECARBOXYLASE
PEPTIDES
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 716,909
FILING DATE: 18-JUN-1991
APPLICATION NUMBER: 586,536
FILING DATE: 21-SEP-1990
SEQ ID NO: 9
LENGTH: 23
5475086-9
Query Match 20.0%; Score 5; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ALPRL 8
DB 19 ALPRL 23
RESULT 44
US-08-592-500-36
Sequence 36, Application US/08592500
Patent No. 6005089
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,006
FILING DATE: 10-FEB-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,500
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..24
OTHER INFORMATION: /note= "Tandem Leu-rich repeated
structure for platelet GPV."
US-08-592-500-36
Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ALPRL 8
DB 12 ALPRL 16
RESULT 45
US-08-195-006-36
Sequence 36, Application US/08195006
Patent No. 6083688
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,006
FILING DATE: 10-FEB-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

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Thu Dec 19 17:47:39 2002

Query Match 20.0%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RLIAF 11
DB 2 RLIAF 6

RESULT 47
PCT-US94-07644A-36
Sequence 36, Application PC/TUS9407644A
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07644A
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-003000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..24
OTHER INFORMATION: /note= "Tandem Leu-rich repeated structure for platelet GPV."
FILING DATE: 19920916
PCT-US94-07644A-36

Query Match 20.0%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 48
US-08-452-242-1
Sequence 1, Application US/08452242
Patent No. 5935795
GENERAL INFORMATION:
APPLICANT: LIN LEU-PEN; COLLINS, FRANKLIN D.;
APPLICANT: DOHERTY, DANIEL H.; LILE, JACK; BEKTESH,
APPLICANT: SUSAN
TITLE OF INVENTION: Glial Derived Neurotrophic Factor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..24
OTHER INFORMATION: /note= "Tandem Leu-rich repeated structure for platelet GPV."
US-08-195-006-36

Query Match 20.0%; Score 5; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 4 ALPRL 8
DB 12 ALPRL 16

RESULT 46
PCT-US92-07865-3
Sequence 3, Application PC/TUS9207865
GENERAL INFORMATION:
APPLICANT: Dreesman, Gordon R.
APPLICANT: Burk, Kenneth H.
APPLICANT: Pauletti, Daniel
TITLE OF INVENTION: Peptide-Based Hepatitis C Virus
TITLE OF INVENTION: Immunoassays
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIORITY APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 1600-0086.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: DP3, amino acids 1917 to 1940 of the
INDIVIDUAL ISOLATE: HCV polypeptide
PCT-US92-07865-3

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

CITY: Englewood
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/452,242
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/182,183
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: 07/788,423
 FILING DATE: 06-NOV-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/774,109
 FILING DATE: 08-OCT-1991
 APPLICATION NUMBER: 07/764,685
 FILING DATE: 20-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/855,413
 FILING DATE: 19-MARCH-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: SYNE-225C4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FRAGMENT TYPE: N-terminal fragment
 US-08-452-242-1

Query Match 20.0%; Score 5; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 7 AALPR 11

RESULT 49
 US-08-934-741A-23
 Sequence 23, Application US/08934741A
 Patent No. 5977298
 GENERAL INFORMATION:
 APPLICANT: Shibata, Kenji
 APPLICANT: Yamasaki, Motoo
 APPLICANT: Yamada, Masako
 APPLICANT: Tamaoki, Tatsuya
 APPLICANT: Kosaka, No. 5977298uo
 APPLICANT: Sato, Soichiro
 TITLE OF INVENTION: NOVEL CALCITONIN DERIVATIVES
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Antonelli, Terry, Stout, & Kraus, LLP
 STREET: Suite 1800, 1300 No. 5977298th Seventeenth Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22209
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM-PC
 OPERATING SYSTEM: DOS
 SOFTWARE: Word Perfect; Version #5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,741A
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 061026/95
 FILING DATE: 20-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Solomon, William I.
 REGISTRATION NUMBER: 28,565
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-312-6600
 TELEFAX: 703-312-6666
 TELEX:
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 25
 IDENTIFICATION METHOD: by experiment
 OTHER INFORMATION: /label=Xaa at location 25
 OTHER INFORMATION: /note= L-prolinamide
 US-08-934-741A-23

Query Match 20.0%; Score 5; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
 DB 13 AALPR 17

RESULT 50
 US-08-453-176A-1
 Sequence 1, Application US/08453176A
 Patent No. 6015572
 GENERAL INFORMATION:
 APPLICANT: LIN, LEU-PEN
 APPLICANT: COLLINS, FRANKLIN D.
 APPLICANT: DOHERTY, DANIEL H.
 APPLICANT: LILE, JACK
 APPLICANT: BEKTESH, SUSAN
 TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic
 TITLE OF INVENTION: Factor
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: One Amgen Center Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: 7.1
 SOFTWARE: Microsoft Word for WIN 7.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/453,176A
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/182,183
 FILING DATE: 23-MAY-1994
 INFORMATION FOR SEQ ID NO: 1:

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

TITLE OF INVENTION: Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,268A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/453,176

FILING DATE:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-935-268A-1

Query Match 20.0%; Score 5; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

Db 7 AALPR 11

RESULT 51

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-453-176A-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

Db 7 AALPR 11

RESULT 51

US-08-451-374-1

Sequence 1, Application US/08451374

Patent No. 6093802

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

APPLICANT: BEKTESH, SUSAN

TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic

TITLE OF INVENTION: Factor

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: 7.1

SOFTWARE: Microsoft Word for WIN 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/451,374

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/182,183

FILING DATE: 23-MAY-1994

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

FRAGMENT TYPE: N-terminal fragment

US-08-451-374-1

Query Match 20.0%; Score 5; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7

Db 7 AALPR 11

RESULT 52

US-08-935-268A-1

Sequence 1, Application US/08935268A

Patent No. 621376

GENERAL INFORMATION:

APPLICANT: LIN, LEU-FEN

APPLICANT: COLLINS, FRANKLIN D.

APPLICANT: DOHERTY, DANIEL H.

APPLICANT: LILE, JACK

us-09-441-061-2.ra1

Thu Dec 19 17:47:39 2002

```

; TOPOLOGY: linear
; FRAGMENT TYPE: N-terminal fragment
US-08-452-229-1

Query Match
Best Local Similarity 20.0%; Score 5; DB 4; Length 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALPR 7
Db 7 AALPR 11

RESULT 54
US-08-785-247-6
; Sequence 6, Application US/08785247
; Patent No. 6040149
; GENERAL INFORMATION:
; APPLICANT: Kolesnick, Richard N.
; APPLICANT: Liu, Jun
; APPLICANT: Zhang, Yuhua
; TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
; TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
; TITLE OF INVENTION: SUPPRESSOR OF RAS, AND METHODS OF USING SAID AGENTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,247
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48582-A/JPW/CCA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-381-0526
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-785-247-6

Query Match
Best Local Similarity 16.0%; Score 4; DB 3; Length 4;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AALP 6
Db 1 AALP 4

RESULT 55
US-08-484-192-2
; Sequence 2, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APATERS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-192-2

Query Match
Best Local Similarity 16.0%; Score 4; DB 1; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PELI 9
Db 2 PELI 5

Search completed: December 19, 2002, 17:44:23
Job time : 15 secs

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us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

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QM protein - protein search, using sw model

Run on: December 19, 2002, 17:43:10 ; Search time 11 seconds
(without alignments)
38.039 Million cell updates/sec

Title: US-09-441-061-2

Perfect score: 25
Sequence: 1 GWAUPLRIATSEHSHFLKGA 25

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Gapop 60.0 , Gapext 60.0

Searched: 106657 seqs, 16763532 residues

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Total number of hits satisfying chosen parameters: 36679

Minimum DB seq length: 0
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Post-processing: Listing first 75 summaries

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5: /cgn2_6/ptodata/2/pubaa/US07 NEW PUB.pap:
6: /cgn2_6/ptodata/2/pubaa/US07 PUBCOMB.pap:
7: /cgn2_6/ptodata/2/pubaa/PCTUS PUBCOMB.pap:
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9: /cgn2_6/ptodata/2/pubaa/US09 NEW PUB.pap:
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13: /cgn2_6/ptodata/2/pubaa/US60 NEW PUB.pap:
14: /cgn2_6/ptodata/2/pubaa/US60 PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	US-08-981-824-29
2	25	20.0	9	10	US-09-894-018-213
3	5	20.0	15	9	US-10-074-257-6
4	5	20.0	21	10	US-09-839-447A-70
5	5	20.0	21	10	US-09-839-447A-73
6	5	20.0	21	10	US-09-917-340-24
7	5	20.0	25	10	US-09-864-761-34001
8	4	16.0	8	9	US-09-826-230-363
9	4	16.0	8	10	US-09-244-694-186
10	4	16.0	9	10	US-09-739-307-101
11	4	16.0	9	10	US-09-760-599-7
12	4	16.0	9	10	US-09-760-599-23
13	4	16.0	9	10	US-09-005-243-69
14	4	16.0	9	10	US-09-224-683-69
15	4	16.0	9	10	US-09-834-765-30
16	4	16.0	4	16.0	US-08-424-550B-278
17	4	16.0	10	10	US-09-834-765-65
18	4	16.0	10	10	US-09-834-765-305
19	4	16.0	10	10	US-09-922-261-9

ALIGNMENTS

RESULT 1
US-08-981-824-29
; Sequence 29, Application US/08981824
; Patent No. US20020114816A1
; GENERAL INFORMATION:
; APPLICANT: ENDL, Josef
; APPLICANT: STAHL, Peter
; APPLICANT: ALBERT, Winfried
; APPLICANT: SCHENDEL, Dolores
; APPLICANT: BOITARD, Christian
; APPLICANT: VAN ENDERT, Peter
; APPLICANT: JUNG, Gunther-Gerhard

20	4	16.0	11	10	US-09-984-055-86	Sequence 86, Appl
21	4	16.0	11	10	US-09-984-057-86	Sequence 86, Appl
22	4	16.0	12	10	US-09-873-459A-37	Sequence 37, Appl
23	4	16.0	12	10	US-09-879-257A-4	Sequence 4, Appl
24	4	16.0	12	10	US-09-765-614B-16	Sequence 16, Appl
25	4	16.0	12	10	US-09-925-715-17	Sequence 17, Appl
26	4	16.0	12	10	US-09-909-950-10	Sequence 10, Appl
27	4	16.0	12	10	US-09-071-838-191	Sequence 191, Appl
28	4	16.0	13	10	US-09-895-072-52	Sequence 52, Appl
29	4	16.0	13	10	US-09-986-552-52	Sequence 11, Appl
30	4	16.0	13	12	US-10-156-820-11	Sequence 11, Appl
31	4	16.0	14	10	US-09-873-459A-38	Sequence 38, Appl
32	4	16.0	14	10	US-09-883-825-29	Sequence 29, Appl
33	4	16.0	15	10	US-09-791-171-82	Sequence 82, Appl
34	4	16.0	15	10	US-09-894-018-272	Sequence 272, Appl
35	4	16.0	15	10	US-09-972-105-1	Sequence 82, Appl
36	4	16.0	16	9	US-09-805-301-82	Sequence 15, Appl
37	4	16.0	16	10	US-09-746-742-15	Sequence 15, Appl
38	4	16.0	16	10	US-09-746-742-18	Sequence 18, Appl
39	4	16.0	16	10	US-09-746-742-38	Sequence 38, Appl
40	4	16.0	17	9	US-09-984-245-297	Sequence 297, Appl
41	4	16.0	17	9	US-09-996-634-94	Sequence 94, Appl
42	4	16.0	17	9	US-09-996-634-95	Sequence 95, Appl
43	4	16.0	17	10	US-09-729-402-1	Sequence 1, Appl
44	4	16.0	18	9	US-09-117-846-46	Sequence 46, Appl
45	4	16.0	18	10	US-09-864-761-35272	Sequence 35272, A
46	4	16.0	18	10	US-09-746-742-17	Sequence 17, Appl
47	4	16.0	18	10	US-09-746-742-19	Sequence 19, Appl
48	4	16.0	18	10	US-09-746-742-38	Sequence 38, Appl
49	4	16.0	18	10	US-09-746-742-39	Sequence 39, Appl
50	4	16.0	18	10	US-09-746-742-40	Sequence 40, Appl
51	4	16.0	18	10	US-09-746-742-41	Sequence 41, Appl
52	4	16.0	18	10	US-09-746-742-55	Sequence 55, Appl
53	4	16.0	18	10	US-09-746-742-64	Sequence 64, Appl
54	4	16.0	18	10	US-09-746-742-65	Sequence 65, Appl
55	4	16.0	18	10	US-09-746-742-67	Sequence 67, Appl
56	4	16.0	18	10	US-09-746-742-68	Sequence 68, Appl
57	4	16.0	19	10	US-09-864-761-35260	Sequence 35260, A
58	4	16.0	19	10	US-09-864-761-36761	Sequence 36761, A
59	4	16.0	19	10	US-09-864-761-39096	Sequence 39096, A
60	4	16.0	20	9	US-09-938-497-2	Sequence 2, Appl
61	4	16.0	20	10	US-09-746-742-43	Sequence 43, Appl
62	4	16.0	20	10	US-09-746-742-45	Sequence 45, Appl
63	4	16.0	20	10	US-09-746-742-46	Sequence 46, Appl
64	4	16.0	20	10	US-09-746-742-48	Sequence 48, Appl
65	4	16.0	20	10	US-09-746-742-49	Sequence 49, Appl
66	4	16.0	20	10	US-09-746-742-51	Sequence 51, Appl
67	4	16.0	20	10	US-09-746-742-53	Sequence 53, Appl
68	4	16.0	20	10	US-09-746-742-56	Sequence 56, Appl
69	4	16.0	20	10	US-09-746-742-66	Sequence 66, Appl
70	4	16.0	21	9	US-10-012-896-986	Sequence 986, Appl
71	4	16.0	21	10	US-09-864-761-33410	Sequence 33410, A
72	4	16.0	22	9	US-10-117-057-10	Sequence 10, Appl
73	4	16.0	22	10	US-09-005-243-75	Sequence 75, Appl
74	4	16.0	22	10	US-09-005-243-76	Sequence 76, Appl
75	4	16.0	22	10	US-09-224-683-75	Sequence 75, Appl

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Thu Dec 19 17:47:41 2002

us-09-441-061-2.rapb

TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID

TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUTAMIC ACID
 FILE REFERENCE: 564-7029
 CURRENT APPLICATION NUMBER: US/08/981,824
 CURRENT FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: PCT/EP96/03093
 EARLIER FILING DATE: 1996-07-15
 EARLIER APPLICATION NUMBER: DE/195 25 784.7
 EARLIER FILING DATE: 1995-07-14
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 29
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-981-824-29

Query Match 100.0%; Score 25; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7e-20;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMAALPRLIAFTSEHSHFSLKKGAA 25
 DB 1 GMAALPRLIAFTSEHSHFSLKKGAA 25

RESULT 2

US-09-894-018-213
 Sequence 213, Application US/09894018
 Patent No. US20020119127A1
 GENERAL INFORMATION:
 APPLICANT: EPIMUNE, Inc.
 APPLICANT: Sette, Alessandro
 APPLICANT: Chestnut, Robert
 APPLICANT: Livingston, Brian
 APPLICANT: Baker, Deniaw
 APPLICANT: Newman, Mark
 APPLICANT: Brown, David

TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 FILE REFERENCE: 39963-20033.00
 CURRENT APPLICATION NUMBER: US/09/894,018
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: PCT/US00/35568
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: US 60/173,390
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: US 60/284,221
 OR FILING DATE: 2001-04-16
 NUMBER OF SEQ ID NOS: 368
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 213
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Transgenic mouse
 US-09-894-018-213

Query Match 20.0%; Score 5; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.9e+04;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLIAF 11
 DB 4 RLIAF 8

RESULT 3

US-10-074-257-6
 Sequence 6, Application US/10074257
 Publication No. US20020187147A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Chih-Pin
 APPLICANT: Lin, Wei-Jen

TITLE OF INVENTION: Antigen Specific Recombinant MHC Class II Molecules and Methods
 FILE REFERENCE: 1954-313
 CURRENT APPLICATION NUMBER: US/10/074,257
 CURRENT FILING DATE: 2002-06-18
 PRIOR APPLICATION NUMBER: US 60/268,714
 PRIOR FILING DATE: 2001-02-15
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 6
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo Sapiens and Mus musculus
 US-10-074-257-6

Query Match 20.0%; Score 5; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGAA 25
 DB 1 KKGAA 5

RESULT 4

US-09-839-447A-70
 Sequence 70, Application US/09839447A
 Patent No. US20020058247A1
 GENERAL INFORMATION:
 APPLICANT: Salberg, Matti
 TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 FILE REFERENCE: TRIPEP.020CP1
 CURRENT APPLICATION NUMBER: US/09/839,447A
 CURRENT FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/556605
 PRIOR FILING DATE: 2000-04-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 70
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificial Peptide
 US-09-839-447A-70

Query Match 20.0%; Score 5; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FTSEH 15
 DB 11 FTSEH 15

RESULT 5

US-09-839-447A-73
 Sequence 73, Application US/09839447A
 Patent No. US20020058247A1
 GENERAL INFORMATION:
 APPLICANT: Salberg, Matti
 TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
 TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
 FILE REFERENCE: TRIPEP.020CP1
 CURRENT APPLICATION NUMBER: US/09/839,447A
 CURRENT FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/556605
 PRIOR FILING DATE: 2000-04-21
 NUMBER OF SEQ ID NOS: 111
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 73
 LENGTH: 21
 TYPE: PRT

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificial Peptide
 US-09-839-447A-73

Query Match 20.0%; Score 5; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FTSEH 15
 Db 12 FTSEH 16

RESULT 6

US-09-917-340-24
 ; Sequence 24, Application US/09917340
 ; Patent No. US20020090369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Christopher J.
 ; APPLICANT: McAnulty, Jonathan F.
 ; APPLICANT: Reid, Ted W.
 ; TITLE OF INVENTION: Transplant Media
 ; FILE REFERENCE: TELANT-06468
 ; CURRENT APPLICATION NUMBER: US/09/917,340
 ; CURRENT FILING DATE: 2001-07-29
 ; PRIOR APPLICATION NUMBER: 60/221,632
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/249,602
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/290,932
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 24
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Misgurnus Anguillicaudatus
 US-09-917-340-24

Query Match 20.0%; Score 5; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 KGA 25
 Db 12 KGA 16

RESULT 7

US-09-864-761-34001
 ; Sequence 34001, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aemica-A-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/532,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27

;; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ;; PRIOR FILING DATE: 2001-01-30
 ;; PRIOR APPLICATION NUMBER: US 60/234,687
 ;; PRIOR FILING DATE: 2000-09-21
 ;; PRIOR APPLICATION NUMBER: US 09/608,408
 ;; PRIOR FILING DATE: 2000-06-30
 ;; PRIOR APPLICATION NUMBER: US 09/774,203
 ;; PRIOR FILING DATE: 2001-01-29
 ;; NUMBER OF SEQ ID NOS: 49117
 ;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ;; SEQ ID NO 34001
 ;; LENGTH: 25
 ;; TYPE: PRT
 ;; ORGANISM: Homo sapiens
 ;; FEATURE:
 ;; OTHER INFORMATION: MAP TO AC006017.2
 ;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
 ;; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 11
 ;; OTHER INFORMATION: EXPRESSED IN HEL1, SIGNAL = 18
 ;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
 ;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.4
 ;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 13
 ;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 17
 ;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
 ;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.7
 ;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13
 ;; OTHER INFORMATION: EST HUMAN HIT: AA332025.1, EVALUATE 4.00e-08
 ;; OTHER INFORMATION: EST_HUMAN HIT: AW965281.1, EVALUATE 3.00e-08
 US-09-864-761-34001

Query Match 20.0%; Score 5; DB 10; Length 25;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 SEHSH 17
 Db 14 SEHSH 18

RESULT 8

US-09-826-290-363
 ; Sequence 363, Application US/09826290
 ; Patent No. US20020164668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Durham, L. Kathryn
 ; APPLICANT: Friedman, David L.
 ; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
 ; APPLICANT: Kimmel, Lida H.
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Potter, David M.
 ; APPLICANT: Rohlf, Christian
 ; APPLICANT: Silber, B. Michael
 ; APPLICANT: Stiger, Thomas R.
 ; APPLICANT: Sunderland, P. Trey
 ; APPLICANT: Townsend, Robert Reid

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

```

; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 363
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-363

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Query Match 16.0%; Score 4; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

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QY 2 MAAL 5
Db 4 MAAL 7

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RESULT 9
US-09-244-694-186
; Sequence 186, Application US/09244694
; Patent No. US2002026037A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Olsen, Henrik S.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 3
; FILE REFERENCE: 1488.1040003
; CURRENT APPLICATION NUMBER: US/09/244,694
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 09/132,088
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/033,662
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: US 08/469,641
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 186
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-694-186

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Query Match 16.0%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

QY 2 MAAL 5
Db 1 MAAL 4

```

```

RESULT 10
US-09-739-907-101
; Sequence 101, Application US/09739907
; Patent No. US20010012889A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/739,907

```

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; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-739-907-101

```

```

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

QY 19 SLKK 22
Db 4 SLKK 7

```

```

RESULT 11
US-09-760-599-7
; Sequence 7, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1C1P
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-7

```

```

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

```

```

QY 6 PRLL 9
Db 5 PRLL 8

```

```

RESULT 12
US-09-760-599-23
; Sequence 23, Application US/09760599
; Patent No. US20010034326A1
; GENERAL INFORMATION:
; APPLICANT: Larson Mr., Richard S.
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
; FILE REFERENCE: SCI200/4-1C1P
; CURRENT APPLICATION NUMBER: US/09/760,599
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

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Thu Dec 19 17:47:41 2002

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-760-599-23

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRLI 9
Db 5 PRLI 8

RESULT 13
US-09-005-243-69
Sequence 69, Application US/09005243
Patent No. US2002018763A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34465
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-005-243-69

Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
Db 2 SLKK 5

RESULT 14
US-09-224-683-69
Sequence 69, Application US/09224683
Patent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

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Thu Dec 19 17:47:41 2002

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-224-683-69
Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 19 SLKK 22
Db 2 SLKK 5

RESULT 15
US-09-834-765-30
Sequence 30, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovics
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
AND DETECTION OF CANCER
FILE REFERENCE: 129.6USU1
CURRENT APPLICATION NUMBER: US/09/834,765
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-30
Query Match 16.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 6 PRLI 9
Db 4 PRLI 7

RESULT 16
US-08-424-550B-278
Sequence 278, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSAHWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL

COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/424,550B
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-278
Query Match 16.0%; Score 4; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 LPRL 8
Db 3 LPRL 6

RESULT 17
US-09-834-765-65
Sequence 65, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovics
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
AND DETECTION OF CANCER
FILE REFERENCE: 129.6USU1
CURRENT APPLICATION NUMBER: US/09/834,765
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-65
Query Match 16.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 6 PRLI 9
Db 4 PRLI 7

RESULT 18
US-09-834-765-305
Sequence 305, Application US/09834765

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Thu Dec 19 17:47:41 2002

```
/ Patent No. US20020055478A1
/ GENERAL INFORMATION:
/ APPLICANT: Mary Paris
/ APPLICANT: Pia M. Challita-Eid
/ APPLICANT: Arthur B. Raitano
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Ava Jakobovits
/ TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
/ TITLE OF INVENTION: AND DETECTION OF CANCER
/ FILE REFERENCE: 129 6USU1
/ CURRENT APPLICATION NUMBER: US/09/834,765
/ CURRENT FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/197,647
/ PRIOR FILING DATE: 2000-04-12
/ NUMBER OF SEQ ID NOS: 770
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 305
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-834-765-305

Query Match      16.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PRLI 9
Db      4 PRLI 7

RESULT 19
US-09-922-261-9
/ Sequence 9, Application US/09922261
/ Patent No. US2002011471A1
/ GENERAL INFORMATION:
/ APPLICANT: COGENT NEUROSCIENCE, Inc.
/ APPLICANT: Lo. Donald C.
/ APPLICANT: Barney, Shawn
/ APPLICANT: Thomas, Mary Beth
/ APPLICANT: Portbury, Stuart D.
/ APPLICANT: Puranam, Kasturi
/ APPLICANT: Katz, Lawrence C.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
/ TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
/ TITLE OF INVENTION: CELL DEATH
/ FILE REFERENCE: 10001-005-999
/ CURRENT APPLICATION NUMBER: US/09/922,261
/ CURRENT FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US/09/461,697
/ PRIOR FILING DATE: 1999-12-14
/ NUMBER OF SEQ ID NOS: 466
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-922-261-9

Query Match      16.0%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AALP 6
Db      3 AALP 6

RESULT 20
US-09-984-056-86
/ Sequence 86, Application US/09984056
/ Patent No. US20020120106A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: BOGOCH, ELENORE S.
/ TITLE OF INVENTION: ANTHRAZ AND SMALL POX REPLICINS AND METHODS OF USE
/ FILE REFERENCE: 09425-46903
/ CURRENT APPLICATION NUMBER: US/09/984,056
/ CURRENT FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 60/303,396
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 60/278,761
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 09/146,755
/ PRIOR FILING DATE: 1998-09-04
/ PRIOR APPLICATION NUMBER: 09/817,144
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 08/198,139
/ PRIOR FILING DATE: 1994-02-17
/ NUMBER OF SEQ ID NOS: 103
/ SOFTWARE: PatentIn 2.1
/ SEQ ID NO 86
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-984-056-86

Query Match      16.0%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ALPR 7
Db      7 ALPR 10

RESULT 21
US-09-984-057-86
/ Sequence 86, Application US/09984057
/ Patent No. US20020151677A1
/ GENERAL INFORMATION:
/ APPLICANT: BOGOCH, ELENORE S.
/ TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
/ TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
/ FILE REFERENCE: 09425-46902
/ CURRENT APPLICATION NUMBER: US/09/984,057
/ CURRENT FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 60/303,396
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 60/278,761
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 09/146,755
/ PRIOR FILING DATE: 1998-09-04
/ PRIOR APPLICATION NUMBER: 09/817,144
/ PRIOR FILING DATE: 2001-03-27
/ PRIOR APPLICATION NUMBER: 08/198,139
/ PRIOR FILING DATE: 1994-02-17
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: PatentIn 2.1
/ SEQ ID NO 86
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-984-057-86

Query Match      16.0%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ALPR 7
Db      7 ALPR 10
```

Thu Dec 19 17:47:41 2002

```

; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Dabsyl-Tyr
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: RGDS chain linked via NH2 group
; OTHER INFORMATION: of lysine
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Branched core
; OTHER INFORMATION: peptide comprising a dabsylated
; OTHER INFORMATION: atherosclerotic
; OTHER INFORMATION: plaque-binding sequence and
; OTHER INFORMATION: RGDS
; US-09-765-614B-16

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 20 LKKG 23
Db 8 LKKG 11

```

RESULT 25

```

US-09-925-715-17
; Sequence 17, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Core peptide
; OTHER INFORMATION: comprising dabsylated-atherosclerotic plaque
; OTHER INFORMATION: binding sequence and RGDS
; NAME/KEY: MOD RES
; LOCATION: (1)
; OTHER INFORMATION: Dabsylated-tyrosine
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Arg-Gly-Asp-Ser chain linked via NH2 group of
; US-09-925-715-17

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 LKKG 23
Db 8 LKKG 11

```

```

; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HBV
; OTHER INFORMATION: capsid-binding peptide
; US-09-873-459A-37

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 22 KGAA 25
Db 9 KGAA 12

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RESULT 23

```

US-09-879-257A-4
; Sequence 4, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-879-257A-4

```

```

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 20 LKKG 23
Db 1 LKKG 4

```

RESULT 24

```

US-09-765-614B-16
; Sequence 16, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed
; TITLE OF INVENTION: Improvements in or relating to
; diagnostic/therapeutic

```


RESULT 26

US-09-909-950-10
; Sequence 10, Application US/09909950
; Patent No. US20020111299A1
; GENERAL INFORMATION:
; APPLICANT: KOLBE, Hanno V.J.
; RASMUSSEN, Ulla B.
; KREIL, Gunther
; ACHETTER, Tilman
; TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/909,950
; FILING DATE: 23-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/909,950
; FILING DATE: 2001-01-23
; APPLICATION NUMBER: FR 90 07901
; FILING DATE: 29-JUN-1993
; APPLICATION NUMBER: FR 94 00202
; FILING DATE: 11-JAN-1994
; APPLICATION NUMBER: FR 9400062.9
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 017753-071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6520
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..12
; OTHER INFORMATION: /note= "xenoxin-1, alkylated,
; fragment C1(2)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-909-950-10

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 1 SLKK 4

RESULT 27

US-09-071-838-191
; Sequence 191, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.
APPLICANT: Chad, Nir, Tomohiro
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-191

Query Match 16.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 SLKK 22
DB 4 SLKK 7

RESULT 28

US-09-895-072-52
; Sequence 52, Application US/09895072
; Patent No. US2002025550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119US0CONT
; CURRENT APPLICATION NUMBER: US/09/895,072
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 1999-09-14
; PRIOR FILING DATE: 1999-09-14
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-895-072-52

Query Match 16.0%; Score 4; DB 10; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 6 PRLI 9
Db 6 PRLI 9

RESULT 29
US-09-986-552-52
; Sequence 52, Application US/09986552
; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 215098US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; FOR FILING DATE: 2000-08-10
; FOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-552-52

Query Match 16.0%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 6 PRLI 9
Db 6 PRLI 9

RESULT 30
US-10-156-820-11
; Sequence 11, Application US/10156820
; Patent No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mastadenovirus, serotype 2
US-10-156-820-11

Query Match 16.0%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 19 SLKK 22
Db 3 SLKK 6

RESULT 31
US-09-873-459A-38
; Sequence 38, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-38

Query Match 16.0%; Score 4; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 22 KGAA 25
Db 10 KGAA 13

RESULT 32
US-09-883-825-29
; Sequence 29, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

Patent No. US20020119127A1
 GENERAL INFORMATION:
 APPLICANT: EPIMUNE, Inc.
 APPLICANT: Sette, Alessandro
 APPLICANT: Chestnut, Robert
 APPLICANT: Livingston, Brian
 APPLICANT: Baker, Denis
 APPLICANT: Newman, Mark
 APPLICANT: Brown, David
 TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 FILE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 FILE REFERENCE: 39963-20033.00
 CURRENT APPLICATION NUMBER: US/09/894,018
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: PCT/US00/35568
 PRIOR FILING DATE: 2000-12-28
 PRIOR APPLICATION NUMBER: US 60/173,390
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: US 60/284,221
 PRIOR FILING DATE: 2001-04-16
 NUMBER OF SEQ ID NOS: 368
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 272
 LENGTH: 15
 TYPE: PRT
 ORGANISM: P. falciparum
 US-09-894-018-272

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 12 SLKK 15

RESULT 35
 US-09-972-105-1
 Sequence 1, Application US/09972105
 Patent No. US20020127616A1
 GENERAL INFORMATION:
 APPLICANT: Burchell, Ann
 APPLICANT: Hume, Robert
 TITLE OF INVENTION: Prenatal Diagnostic Methods
 TITLE OF INVENTION: Cross-References
 FILE REFERENCE: 350013-76
 CURRENT APPLICATION NUMBER: US/09/972,105
 CURRENT FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: US 09/392,055
 PRIOR FILING DATE: 1999-09-09
 PRIOR APPLICATION NUMBER: PCT/GB98/00656
 PRIOR FILING DATE: 1998-03-03
 PRIOR APPLICATION NUMBER: US 60/067,520
 PRIOR FILING DATE: 1997-12-04
 PRIOR APPLICATION NUMBER: GB 9704876.3
 PRIOR FILING DATE: 1997-03-08
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Human
 US-09-972-105-1

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 11 SLKK 14

ATTORNEY/AGENT INFORMATION:
 NAME: No. US20020151024Aland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/30822
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-893-825-29

Query Match 16.0%; Score 4; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 19 SLKK 22
 DB 11 SLKK 14

RESULT 33
 US-09-791-171-82
 Sequence 82, Application US/09791171
 Patent No. US20020094336A1
 GENERAL INFORMATION:
 APPLICANT: ANDERSEN, Peter
 APPLICANT: NIELSEN, Rikke
 APPLICANT: OETTINGER, Thomas
 APPLICANT: RASMUSSEN, Peter Birk
 APPLICANT: ROSENKRANDS, Ida
 APPLICANT: WELDLING, Karin
 APPLICANT: FLORIO, Walter
 TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
 FILE REFERENCE: 670001-2002.1
 CURRENT APPLICATION NUMBER: US/09/791,171
 CURRENT FILING DATE: 2001-02-20
 PRIOR APPLICATION NUMBER: 09/050,739
 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 0376/97
 PRIOR FILING DATE: 1997-04-02
 PRIOR APPLICATION NUMBER: 1277/97
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/044,624
 PRIOR FILING DATE: 1997-04-18
 PRIOR APPLICATION NUMBER: 60/070,488
 PRIOR FILING DATE: 1998-01-05
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 82
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Mycobacterium tuberculosis
 US-09-791-171-82

Query Match 16.0%; Score 4; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 AALP 6
 DB 8 AALP 11

RESULT 34
 US-09-894-018-272
 Sequence 272, Application US/09894018

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

/ CURRENT APPLICATION NUMBER: US/09/746,742
 / CURRENT FILING DATE: 2000-12-21
 / PRIOR APPLICATION NUMBER: PCT/US99/17351
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: US 60/043,280
 / PRIOR FILING DATE: 1997-04-17
 / PRIOR APPLICATION NUMBER: US 09/062,241
 / PRIOR FILING DATE: 1998-04-17
 / PRIOR APPLICATION NUMBER: US 60/094,676
 / PRIOR FILING DATE: 1998-07-30
 / PRIOR APPLICATION NUMBER: US 60/100,265
 / PRIOR FILING DATE: 1998-09-14
 / PRIOR APPLICATION NUMBER: US 60/101,058
 / PRIOR FILING DATE: 1998-09-18
 / PRIOR APPLICATION NUMBER: US 60/132,295
 / PRIOR FILING DATE: 1999-05-03
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWARE: Fast-SEQ for Windows Version 4.0
 / SEQ ID NO 15
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: D-peptide
 / US-09-746-742-15

Query Match 16.0%; Score 4; DB 10; Length 16;
 Best Local Similarity 100.0%; Pred. No. 28+02; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 KKGGA 24
 DB 1 KKGGA 4

RESULT 38
 US-09-746-742-16
 / Sequence 16, Application US/09746742
 / Patent No. US20020077284A1
 / GENERAL INFORMATION:
 / APPLICANT: Eckert, Deborah M.
 / APPLICANT: Chan, David C.
 / APPLICANT: Malashkevich, Vladimir
 / APPLICANT: Cart, Peter A.
 / APPLICANT: Kim, Peter S.
 / TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
 / FILE REFERENCE: 0399.1192-008
 / CURRENT APPLICATION NUMBER: US/09/746,742
 / CURRENT FILING DATE: 2000-12-21
 / PRIOR APPLICATION NUMBER: PCT/US99/17351
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: US 60/043,280
 / PRIOR FILING DATE: 1997-04-17
 / PRIOR APPLICATION NUMBER: US 09/062,241
 / PRIOR FILING DATE: 1998-04-17
 / PRIOR APPLICATION NUMBER: US 60/094,676
 / PRIOR FILING DATE: 1998-07-30
 / PRIOR APPLICATION NUMBER: US 60/100,265
 / PRIOR FILING DATE: 1998-09-14
 / PRIOR APPLICATION NUMBER: US 60/101,058
 / PRIOR FILING DATE: 1998-09-18
 / PRIOR APPLICATION NUMBER: US 60/132,295
 / PRIOR FILING DATE: 1999-05-03
 / NUMBER OF SEQ ID NOS: 68
 / SOFTWARE: Fast-SEQ for Windows Version 4.0
 / SEQ ID NO 16
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: D-peptide
 / US-09-746-742-16

RESULT 36
 US-09-805-301-82
 / Sequence 82, Application US/09805301
 / Patent No. US20020173456A1
 / GENERAL INFORMATION:
 / APPLICANT: Smith, Louis C.
 / APPLICANT: Sparrow, James T.
 / APPLICANT: Hauer, Jochen
 / APPLICANT: Mims, Martha P.
 / TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 / MACROMOLECULE DELIVERY
 / NUMBER OF SEQUENCES: 139
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Lyon & Lyon
 / STREET: 633 West Fifth Street
 / SUITE: Suite 4700
 / CITY: Los Angeles
 / STATE: California
 / COUNTRY: U.S.A.
 / ZIP: 90071-2066
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 / storage
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: IBM P.C. DOS 6.0
 / SOFTWARE: Word Perfect 6.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/805,301
 / FILING DATE: 12-Mar-2001
 / CLASSIFICATION: <Unknown>
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/584,043
 / FILING DATE: <Unknown>
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Warburg, Richard J.
 / REGISTRATION NUMBER: 32,327
 / REFERENCE/DOCKET NUMBER: 217/189
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (213) 499-1600
 / TELEFAX: (213) 955-0440
 / TELEX: 67-3510
 / INFORMATION FOR SEQ ID NO: 82:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 16 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / SEQUENCE DESCRIPTION: SEQ ID NO: 82:
 / US-09-805-301-82

Query Match 16.0%; Score 4; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 28+02; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 SLKK 22
 DB 2 SLKK 5

RESULT 37
 US-09-746-742-15
 / Sequence 15, Application US/09746742
 / Patent No. US20020077284A1
 / GENERAL INFORMATION:
 / APPLICANT: Eckert, Deborah M.
 / APPLICANT: Chan, David C.
 / APPLICANT: Malashkevich, Vladimir
 / APPLICANT: Cart, Peter A.
 / APPLICANT: Kim, Peter S.
 / TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
 / FILE REFERENCE: 0399.1192-008

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

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Query Match      16.0%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

RESULT 39
US-09-746-742-18
Sequence 18, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-18

Query Match      16.0%; Score 4; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

RESULT 40
US-09-984-245-297
Sequence 297, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/042,344

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PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,350
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,135
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/050,937
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,099
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,352
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,186
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,069
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 297
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-297

Query Match      16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MAAL 5
Db 1 MAAL 4

RESULT 41
US-09-996-634-94
Sequence 94, Application US/09996634
Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28

```

us-09-441-061-2.rapb

Thu Dec 19 17:47:41 2002

Acetylhydrolase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,402
FILING DATE: 04-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 08-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. US20010021379Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-729-402-1

Query Match 16.0%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPRL 11
DB 14 LPRL 17

RESULT 44
US-10-117-846-46
Sequence 46, Application US/10117846
Patent No. US20020168673A1
GENERAL INFORMATION:
APPLICANT: Fuller, Margaret T
APPLICANT: Hales, Karen G.
APPLICANT: Santei, Ansgar H.
TITLE OF INVENTION: Microfusions, Fzo Homologs and Functional
FILE REFERENCE: STAN-063CIP3
CURRENT APPLICATION NUMBER: US/10/117,846
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/413,285
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: PCT/US00/27871
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-846-46

us-09-996-634-95

PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 94
LENGTH: 17
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis

Query Match 16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
DB 8 LPRL 11

RESULT 42
US-09-996-634-95
Sequence 95, Application US/09996634
Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 95
LENGTH: 17
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis

Query Match 16.0%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
DB 4 LPRL 7

RESULT 43
US-09-729-402-1
Sequence 1, Application US/09729402
Patent No. US20010021379A1
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EST_HUMAN HIT: AA832005.1, EVALUATE 7.00e-04
US-09-864-761-39272

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LPRL 8
Db 9 LPRL 12

RESULT 46
US-09-746-742-17
Sequence 17, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-17

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 3 KKGA 6

RESULT 47
US-09-746-742-19
Sequence 19, Application US/09746742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EST_HUMAN HIT: AA832005.1, EVALUATE 7.00e-04
US-09-864-761-39272

Query Match 16.0%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLJA 10
Db 14 RLJA 17

RESULT 45
US-09-864-761-39272
Sequence 39272, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenshang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aescmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotax Sequence Listing Engine vers. 1.1
SEQ ID NO 39272
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004583.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EST_HUMAN HIT: AA832005.1, EVALUATE 7.00e-04
US-09-864-761-39272

Query Match 16.0%; Score 4; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
ID NO 19
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-19

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 21 KKGa 24
Db 1 KKGa 4

RESULT 48
US-09-746-742-38
Sequence 38, Application US/09/746,742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-39

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 21 KKGa 24
Db 1 KKGa 4

RESULT 50
US-09-746-742-40
Sequence 40, Application US/09/746,742
Patent No. US20020077284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-38

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PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-40

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 51
US-09-746-742-41
Sequence 41, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
US-09-746-742-41

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 52
US-09-746-742-55
Sequence 55, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/132,295
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D-peptide
NAME/KEY: VARIANT
LOCATION: (1)...(18)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-746-742-55

Query Match
Best Local Similarity 16.0%; Score 4; DB 10; Length 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKG 24
DB 1 KKG 4

RESULT 53
US-09-746-742-64
Sequence 64, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399.1192-008
CURRENT APPLICATION NUMBER: US 09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17

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Db 1 KKGA 4

RESULT 55
US-09-746-742-67
; Sequence 67, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION: Deborah M.
; APPLICANT: Eckert, David C.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-67

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

Search completed: December 19, 2002, 17:45:00
Job time: 11 secs

PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-64

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4

RESULT 54
US-09-746-742-55
; Sequence 65, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-65

Query Match 16.0%; Score 4; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KKGA 24
Db 1 KKGA 4